EXHIBIT A

SEQ NO 11, 13, 15, 16 and 17 against SEQ NO 1

									S	Section 1
SEO ID NO 1	(1) 1 (1) CACAC	10 10 ATAGGCTAGG	1) 1 10 10 20 11 10 11 11 11 11 11 11 11 11 11 11 11	30	40 ATCATGGACC	50 FGTGTTATAA	60 FABATATGTT	70 TAATTGTGCT	30 40 50 60 70 80 91	91
SEQ ID NO 11 SEQ ID NO 13))							;
SEQ ID NO 16 SEQ ID NO 17 Consensus	(E)									
	(92) 92	100	110	120	130	140	150	160	170	3eciloii 2 182
SEQ ID NO 1	(92) AAGTC	CTGATGTTAG	(92) AAGICCIGAIGIIAGIIGCCIIGAA	GICAGACACC	CAGAGAGAAT	CACAGGITII	CAGATTAATT	CATCGCTIGA	GTCAGACACCCAGAGAATCACAGGTTTTCAGATTAATTCATCGCTTGATTCTTATCCCTGAAGT	GAAGI
SEQ ID NO 13	(E) - (E) - (E)									
SEQ ID NO 16	(E)									
SEQ ID NO 17 Consensus	(92)					 	 	 		igo
	(183) 183	190	200	210	220	230	240	250	260	273
SEQ ID NO 1	(183) CATAT	CTCTGGATCT	GGTT	CATTATAAAT	CATTATAAATTTCAATGATTCTTTT	([─	ATGGCCATGI	CATICATAIC	CTATAIGGCCAIGICAIICAIAICCIGIGIAAIAIGGGGA	GGGGA
SEQ ID NO 13										
SEC ID NO 15	(1) 									
SEQ ID NO 17	(1)			1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	1 1 1 1 1 1 1					
Consensus	(183)									

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SEQ NO 11, 13, 15, 16 and 17 against SEQ NO 1

										Section 4
SEQ ID NO 1		280 GAGGTATGA	290 ATGACATCATI	300 TCAAAAAGCA	310 CCIGCAAITI	320 TITTITGCCA	330 AAGCACTTACA	340 GCTTTTTCTC	(274) 274 280 290 300 310 320 320 330 340 350 350 364 280 (274) AACTGAGGTATTCTCATGTTGCTTTCAAAAGT	364 AAAGT
SEQ ID NO 11 SEQ ID NO 13 SEQ ID NO 15	(E) (E) (E) (E) (F)									
SEQ ID NO 16 SEQ ID NO 17 Consensus	(1) (1) (274)									
	(365) 365	370	380	390	400	410	420	430	440	455
SEQ ID NO 1	(365) CAIT	GAAATATIG	TTCACATATT	TIGCAGAIGA	.GGAAATGAA1	TATTCAAATGC	ATTAGGTATC	TIGICCAAGI	(365) CATTGAAATATTGTTCACATATTTTGCAGATGAGGAAATGAATATTCAAATGCATTAGGTATCTTGTCCAAGTTCTTACAGCCAGAAAGTA	AAGTA
SEQ ID NO 11 SEQ ID NO 13	(1)									
SEQ ID NO 15 SEQ ID NO 16	(1)									
SEQ ID NO 17	(1)									
	()								S	Section 6
	(456) 456		470	480	490	200	510	520	530	546
SEQ ID NO 1	(456) GAGA	AATGAATTT	AATTAC	TCTTCTACCT	CTIGGCTTA1	GCTCTTTTCF	ATGACACTGGG	AATAAATGTC	CITGGCTTATGCTCTTTTCATGACACTGGGAATAAATGTCTGAACAAGCATGACTTCA	CTTCA
SEQ ID NO 13	(1)									
SEQ ID NO 15	(1)					1				1 1 1
SEQ ID NO 16	(1)		.							 - - -
SEQ ID NO 17	(1)									
Consensus	(456)									

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SEQ NO 11, 13, 15, 16 and 17 against SEQ NO 1

	(547) 547	560	570	580	290	600	610	620	Section 7 637
SEQ ID NO 11 SEQ ID NO 11 SEQ ID NO 13 SEQ ID NO 15 SEQ ID NO 16 SEQ ID NO 16	(547) TGTTTCAACTATTTATCAAATACTT(1)	TATITATCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	ATACTIGITI 	TCTACTAAGA	TCTTGCACTC	ACTCAGTGGC	ATCCCCTGAA	AGCCTGCTGAT	GTITICIACIAAGAICIIGCACICAGIGGGAICCCCIGAAGCCIGCIGAITAITIGICCIII
	(638) (638)	650	099	089 079	680	069	007	710	690 700 710 728
SEQ ID NO 11 SEQ ID NO 13 SEQ ID NO 15 SEQ ID NO 16 SEQ ID NO 17 Consensus									
	(729) 729	740	750	760	770	780	790	800	Section 9
SEQ ID NO 1 SEQ ID NO 11 SEQ ID NO 13	(729) ACAGATCAT (1)	ACTCAACAAC?	ATGICIAAIG	TCAGCACACA.	AIGICIAACA	ATCATTTAT6	AATACTTTA:	IGTCAAACATAA	AATGTCAGCACACAATGTCTAACAATCATTTATGAATACTTTATGTCAAACATAAGCAATAACCTA
SEQ ID NO 15 SEQ ID NO 16 SEQ ID NO 17	(T) (T) (T) (T)								
Consensus	(729)								

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SEQ NO 11, 13, 15, 16 and 17 against SEQ NO 1

	(820) 820	α,	830	840	850	860	870	880	890	006	Section 10 910
(820) (320) (320) (320)	(1) ATT	(820) ATTAAGGAAGGTATTTTTAATAAAT (1)	T	TAATAAATTG/	ACACTITITO 	TGACACITITIGACATAACCATATITCAAGIGGCTCCATTGITTTGIT	TATTTCAAGT	GGCTCCATT	GTTTTGTTTF	TTTATTTAT TTTAT TT	TTATITA
99 99	(911) 911 (11) (11) (11) (11) (11) (11) (11) (1	(911) 911 920 930 (911) TITATITATITATITIGAGAAAGG (1)	0 FATTTT	930 GAGAAAGGGT(940 GTCTCACTCTGT		960 1 G G A G T G C A G	950 960 970 980 990 1001 TGCCCAGACTGGAGTGCAACATCATAGCTCACTACAGCCTCGACCTCT	980 CATAGCICAC	990 TACAGCCTC	GACCTCT GACCTCT
9.9	1002) 1002 1002) CIGG (1)	2) 1002 1010 22) CTGGGCTCAAGG (1)(1)	0 GCAATCC 	SEQ ID NO 13 (1)	1030 SCTTCCCAAC	1030 1040 1050 1060 1060 1070 1080 1090 1090 1090 1090 1090 1090 109	1050 CTACAGGIG1	1060 GTACCATCA	1070 TGCCAGGCTA	1080 AATTTTTGT	1092 ATTTTGT
	£ £ £										
=	Consensus (1002)										

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SEQ NO 11, 13, 15, 16 and 17 against SEQ NO 1

	10001	000	7	000	C	7	C U	7	7	Section 13
EQ ID NO 1	(1093) 1093 (1093) AGAGA	1100 .cggggttt	(1093) 1093 1100 1100 SEQ ID NO 1 (1093) AGAGGGGGGTTTTGCCTGGTCGTC	1120 TCCGGGTTGG	1130 TCTCAAACTCO	1140 CIGGGIGIIC	1150 CGCCCACCIT	1160 GGCCTCCCA	1120 1170 1130 1140 1150 1160 1160 1160 1170 1183 CGGGGTTGGCTCCCAAAGTGCTGGGATTATAGGC	1183 TTATAGGC
SEQ ID NO 11 SEQ ID NO 13 SEQ ID NO 15 SEQ ID NO 16										
SECTIONO 17 (1) Consensus (1093)	(1093)	 	 				 	 - - - - - -		
	(1184) 1184	1190	1200	1210	1220	1230	1240	1250	1260	1274
SEQ ID NO 11 SEQ ID NO 11 SEQ ID NO 13 SEQ ID NO 15 SEQ ID NO 16	(1184) ATGAG (1) (1) (1)	CCTCAAGT	SEQ ID NO 1 (1184) ATGAGCCTCAAGTGGCTACTTTTTA SEQ ID NO 11 (1)	TAGGGTTGAA	ATTTATATTG,	ACTGTCAACT	AGCTTCCCTA	GTTAGTATT	GGGTTGAAATTTATATTGACTGTCAACTAGCTTCCCTAGTTAGT	AACTAATT
SEQ ID NO 17 (1) Consensus (1184)	(1184)									
	(1275) 1275 1280	1280	1290	1300	1310	1320	1330	1340	1350	1365
SEQ ID NO 1	(1275) TATAT	TACCATCCA	SEQ ID NO 1 (1275) TATATTACCATCCAACTTGTCAACA	CATTIGITGA	TITGITGAAAIAIAACIGICCICACII	H 1	TTTTGTGTGA.	ACATIGAAT 	TITIGIGIGAACATIGAATACACITICAGACTAAATTI	CTAAATTT
Q ID NO 13		 								
SEC ID NO 15	(1)									
SEQ ID NO 17	(1)						1 1 1 1 1 1 1 1 1			1 1 1 1 1 1
Consensus (1275)	(1275)									

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SEQ NO 11, 13, 15, 16 and 17 against SEQ NO 1

	(19ee) 19ee	000	1300	1400	4440	1400	1430	1440	Section 16
SEQ ID NO 1	33	TACTTAATGTCTT	ATTCTTTATT	AGAGTTAATA	ATATITCITA	ATACTITGCC	TTCCACAAA	TATIAGAGITAATATTICITAATACTTIGCCTICCACAAATGAATAACTIGITIGIGATGGG	TTGTGATGGC
SEQ ID NO 13 SEQ ID NO 15 SEQ ID NO 15 SEQ ID NO 16 SEQ ID NO 16									
Consensus (1366)	(1366)								Section 17
	(1457) 1457	1470	1480	1490	1500	1510	1520	1530	1547
SEQ ID NO 11 SEQ ID NO 11 SEQ ID NO 13 SEQ ID NO 15 SEQ ID NO 16	SEQ ID NO. 1 (1437) I ACCICIII I I I I I I I I I I I I I I				1		CAAAAACAA 	1 G A A A G A A A I A C	
SEQ ID NO 17 (1) Consensus (1457)	(1457)								Section 18
	(1548) 1548	1560	1570	1580	1590	1600	1610	1620	1638
SEQ ID NO 1		3GGGAGGGGTAAA	TGAATATAAT	TCAAAATACC	ATATATTAT	TCAACACTG1	TIGGAATATA	TGTCCTGTTGG/	AAATGTAAAAG
SEQ ID NO 13	(1)								
SEQ ID NO 16	(1)								
SEQ ID NO 17	. (1)								
Consensus (1548)	; (1548)								

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SEQ NO 11, 13, 15, 16 and 17 against SEQ NO 1

									Section 19	on 19
	(1639) 1639	1650	1660	1670	1680	1690	1700	1710		1729
EQ ID NO 1	(16	TGTICICITC	CIGGGICICA	SACITITAGG	ATCTAGTIGA	CAGACTITTAGGATCTAGTTGAGGGAACTGGACTTATACACAAAATACAATTCAACAACATTATGA	CITATACACA	AAATACAATI	CAACAACAII	ATGA
SEQ ID NO 13 SEQ ID NO 13 SEQ ID NO 15 SEO ID NO 15										
SEQ ID NO 17 (1) Consensus (1639)	(1) (1639)									
	0000	1	i i	000		000	001	000	Section 20	on 20
EQ ID NO 1	(1730) GCTAGAA	1/40 AATCCATGAG	CTAAAGTCTT	TGGCAAAGAC	I//U ATTAGGTAAC	I/80 ATGAGGAGTCA	1790 AGGAAAAGGA	18UU GAAATTACTG	TGGGCTGGAA	166T
SEQ ID NO 11 SEQ ID NO 13 SEQ ID NO 15	(E)									
SEQ ID NO 16	(1)									
Consensus (1730)	; (1730)	 		 	 	 		 		21 of
	(1821) 1821	1830	1840	1850	1860	1870	1880	1890	1900	1911
EQ ID NO 1	(182	CATGAGATGG	AGGAAGTGGC	TIGITACIGG	AGAAAGGATG	GCTTGTTACTGGAGAAAGGATGAGGTTCAAAGAGATGGGAAAAAAAA	AGA TGGGAAA?	AAAAGAAAGA	GAGAAGAAAG	AAAA
SEC ID NO 13	(1)									
SEQ ID NO 15	(1)									
Q ID NO 16	(1)									
SEQ ID NO 17	(1)									1 1 1
Consensus (1821)	; (1821)									

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SEQ NO 11, 13, 15, 16 and 17 against SEQ NO 1

	0707	000	000	0	C	3	C C	000	7	Section 22
ID NO 1	(1912) 1912 (1912) GAAAT	1920 GAGGAAAA	(1912) 1912 1920 (1930) SEQ ID NO 1 (1912) GAAATGAGGAAAAACAAGTTGCCAG.	1940 Saaagaacaa	1940 1950 1950 1960 AAAGAACAAGGAAAGCAATITIGCCTAGGAAAGGTAATATAACTAG	1960 AGGCAGGTAA	1970 GCAGTGGATT	1980 TIGCCCIAG	1990 GGAAGGTAAT	2002 ATAACTAG
SEQ ID NO 11 SEQ ID NO 13 SEQ ID NO 15 SEQ ID NO 16 SEQ ID NO 16										
Consensus (1912)	(1912)									Section 23
	(2003) 2003	2010	2020	2030	2040	2050	2060	2070	2080	2093
SEQ ID NO 13 (1) SEQ ID NO 15 (1) SEQ ID NO 16 (1) SEQ ID NO 17 (1) Consensus (2003)	(1) (1) (1) (1) (2003)									Section 24
	(2094) 2094	2100	2110	2120	2130	2140	2150	2160	2170	2184
SEQ ID NO 1	(2094) CATGACAG	CAGTAAATA	TATGTTGGGA	AAAAATAAC 	AAAAATAACCGGTAAACATTTACATCAGCTCTTTTTCCTAAAGAGAAACCTATTCCATGCTATGAA	TIACAICAGC	TCTTTTCCT	AAAGAGAAA	CCTATICCAT	GCTATGAA
SEQ ID NO 13		 	 							
D NO 15	(1)									
SEQ ID NO 17	(1)								1 1 1 1 1 1 1	
Consensus (2094)	(2094)									

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SEQ NO 11, 13, 15, 16 and 17 against SEQ NO 1

		6	6	6		6		1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	4	Section 25
SEQ ID NO 1	(2185) 2185 (2185) ATATI	2190 TIGICACA	(2185) 2185 2190 2200 SEQ ID NO 1 (2185) ATATITGICACAATICIGITITICAA.	2210 CAAAATACTI	2220 IGCICIACIT	2230 TICCAAGCCA	2240 .CAAGAGGAAA	2250 CATITICICI	2210 2220 2220 2230 2240 2276 AATACTIGCICTACTITICCAAGCCACAAGAGGAAACAITIICICIGCCAACACTCICIGACCITA	2275 TGACCITA
SEQ ID NO 11 (1) SEQ ID NO 13 (1) SEQ ID NO 15 (1) SEQ ID NO 16 (1) SEQ ID NO 17 (1)	(1) (1) (2) (3) (4) (4) (4) (4) (4) (4) (4) (4) (4) (4									
Poelioe 100	(2012)									Section 26
	(2276) 2276		2290	2300	2310	2320	2330	2340	2350	2366
SEQ ID NO 11 SEQ ID NO 11 SEQ ID NO 13 SEQ ID NO 15 SEQ ID NO 15	(1) (2276) ACCAG (1) (1) (1)		ACTACGTCTA	CTCTTAAGC	ICTCTTTAGA	SEQ ID NO 1 (2276) ACCAGITICICCACIACGICIACICITIAAGCICITIAGAGCIGIGIGIAICICGICI EQ ID NO 11 (1)		ATGTAAACC	TATGTAAACCTCCTAGATGATATACTTATGG	ACTTATGG
SEQ ID NO 17 (1) Consensus (2276)	(1)									
	(2367) 2367		2380	2390	2400	2410	2420	2430	2440	2457
SEQ ID NO 1 SEQ ID NO 11	(2367) AAATATTCA (1)	ATTCAGGC.	AACTTTTTCA 	TGAACTTTA(CCAGGAAAGA	CATTTCTAGC	AGGAGAGCAT	GAATAGAAA. 	SEQ ID NO 1 (2367) AAATATTCCAGGCAACTTTTCCATGAACTTTACCAGGAAAGACATTTCTAGCAGGAGGCATGAATAGAAATGGACTCTTCCCCAGTCTCTG EQ ID NO 11 (1)	AGTCTCTG
SEQ ID NO 13 SEQ ID NO 15										
SEQ ID NO 16	(1)									
SECTIONO 17 (1) Consensus (2367)	(1): (2367)	 	 			 	 	 	 	

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SEQ NO 11, 13, 15, 16 and 17 against SEQ NO 1

									Section 28
	(2458) 2458	2470	2480	2490	2500	2510	2520	2530	2548
SEQ ID NO 1	_	SIGACIGIGGI	CACTCTAACT	ATAAAAAGTG	TGTAAAAATC	ATGAGCAGAT	TATTTCATT	ICCIIGGGGIC	CCTAAAAATTT
SEQ ID NO 13 SEQ ID NO 13 SEQ ID NO 15 SEQ ID NO 16									
SEQ ID NO 17 (1) Consensus (2458)	7 (1) ; (2458)	 							
	(2549) 2549	2560	2570	2580	2590	2600	2610	2620	2639
SEQ ID NO 1		GTATTAGCAC	AGGAAGAIII	AAATTGATTT	TIAAATIGAITICICAACACATICAGAIAICI	TCAGATATCT	TAIGAACII	rattaagata?	TATTAAGATAAATTTCCTCCAGCA
SEQ ID NO 13									
SEQ ID NO 16	(1)								
Consensus (2549)	; (2549)								Societies S
	(2640) 2640	2650	2660	2670	2680	2690	2700	2710	2720 2730
SEQ ID NO 1	(564	ACTCATATAT	ACAGAATAAA	AAATAAAGCA	GAAAATTAGT	GTACCTGGCT	AAAATGAG	AGCAGGGTICI	ATTTT
SEQ ID NO 11 SEQ ID NO 13	(1)								
SEQ ID NO 15	(1)						! ! ! ! ! ! ! ! ! ! ! ! ! ! ! ! ! ! ! !		
EQ ID NO 16	(1)			 		 			
SEQ ID NO 17	. (1)								
Consensus (2640)	; (2640)								

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SEQ NO 11, 13, 15, 16 and 17 against SEQ NO 1

7020 (1020)	0770	071	0020	02.20	00077	002.0	0000	0,000	Section 31
, A.	2740 actaagacag	(2731) 2731 2730 2750 2750 2770 2780 2790 SEQ ID NO 1 (2731) AAGTCACTAAGACAGTAATAATACATTAATGATGTGT	2760 ATTAATGATA	2770 AAAIGITAAC	2780 ATTAGTTAAT	2790 TATTAGATGT	2800 GITITIGIA	2820 2810 2821 TITIGIAIGCCAGCCACATAATAT	2821 ATAATAT
1 1 1 1 1									Coordina 33
	2830	2840	2850	2860	2870	2880	2890	2900	2912
		EQ ID NO 11 (1)							
	2920	2930	2940	2950	2960	2970	2980	2990	Section 33
9	STIGICICAA	ACTIGGTA	TAGAAAGCAG	TAGAAAGCAGAAACTTTTAGTTATTAAGATTCTTACTATTCCAATATTTGAATAAAACAGTGACCT	TTATTAAGAT	TCTTACTATI	CCAATATIT	GAATAAAACA	GIGACCI
i I									
- !		-							
1									
!									

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SEQ NO 11, 13, 15, 16 and 17 against SEQ NO 1

3094	FTTTATGTT	3185	CAACTITIG	3276	ATGAAAAAA
3080	CATATTAATTTAATTTAATTTAATTTAATTTAATTTAA	3170	TTAACTAAATGIGTTTTGTACCACATTTTGACAACTTTTG	3260	SEQ ID NO 1 (3186) TITTAACTATGATTCAGCTTATAACAAAACAATGCATCTTCTCTCTC
3070	TAACATCTTC	3160	TGTTTTGTA(3250	GGTTAATGA/
3060	GHTTCTAATC	3150	TAACTAAATG	3240	CTGTTAATAA
3050	ATACATCAAAACCTTCTGGCATTAGATGTTTCTAATCTAACATCTTCATATTAATT	3140	\vdash \vdash \vdash \vdash \vdash \vdash \vdash	3230	CTTCTCTCTCTCTCTCTCTCTCTCTTTTTTTTTTTTTT
3040	AAAACCTTCT(3130	CTAAACGCTGGATGCATT	3220	AACAATGCAT
3030	CTGATACATC	3120	TGTGTTT	3210	AACAAAACAAA
3020	SEQ ID NO 1 (3004) GCTAAGAAACCCCAATAATTTCTG. EQ ID NO 11 (1)	3110	SEQ ID NO 1 (3095) TTGATTATCTACATTCAGTAGTGAA EQ ID NO 11 (1)	3200	TTCAGCTTAT
3010	A G A A A C C C C C C C C C C C C C C C	3100	(TTATCTAC		AACTATGA'
(3004) 3004	(3004) GCTP (1) (1) (1) (1) (1) (1)	(3095) 3095 3100	(3095) TIGATTATC (1) (1) (1) (1) (1) (3095)	(3186) 3186	(3186) TTTT (1) (1) (1) (1) (1) (1)
	SEQ ID NO 1 (3004) SEQ ID NO 11 (1) SEQ ID NO 13 (1) SEQ ID NO 15 (1) SEQ ID NO 16 (1) SEQ ID NO 16 (1) SEQ ID NO 17 (1) Consensus (3004)		SEQ ID NO 1 (3095) SEQ ID NO 11 (1) SEQ ID NO 13 (1) SEQ ID NO 15 (1) SEQ ID NO 16 (1) SEQ ID NO 16 (1) SEQ ID NO 17 (1) Consensus (3095)		SEQ ID NO 1 (3186) SEQ ID NO 11 (1) SEQ ID NO 13 (1) SEQ ID NO 15 (1) SEQ ID NO 16 (1) SEQ ID NO 17 (1)

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SEQ NO 11, 13, 15, 16 and 17 against SEQ NO 1

									Section 37
	(3277) 3277	3290	3300	3310	3320	3330	3340	3350	3367
SEQ ID NO 1	_	TIAIGCACAII	: [-1	TCCTIGCTAA	GGATATTAGI	ACTIGACGAT	TCTGTAACAA	TITCCITGCTAAGGATATTAGTACTTGACGATTCTGTAACAAAGAATTATCATGGGATGAAACT	ATGAAACT
SEQ ID NO 13 SEQ ID NO 15 SEQ ID NO 15									
EQ ID NO 17 (1) Consensus (3277)	3 (3277)						 		
	(3368) 3368	3380	3390	3400	3410	3420	3430	3440	3458
SEQ ID NO 11 SEQ ID NO 11 SEQ ID NO 13	SEQ ID NO 1 (3368) TIGATGCAAATATCTTATCAATACA. EQ ID NO 11 (1)	AATATCTTATC 	AATACAATGT 	ATGIGCTTGATITT 	TTACCTAGATGAGATTTTT.	AGATTTTTCTT 	TICTICTIT	TCTTTTTGAGACAGGGTTTTGCT 	GTTTTGCT
SEQ ID NO 15 SEQ ID NO 16 SEQ ID NO 17	(1) (2) (2) (3) (4) (4) (5) (6) (7) (7) (7) (7) (7) (7) (7) (7) (7) (7								
Consensus (3368)	3368)								Section 39
	(3459) 3459	3470	3480	3490	3500	3510	3520	3530	3549
SEQ ID NO 1	1 (3459) GTGTTACCO	CAGGCTAGCCT	CAAACCCCTG	CCCCTGGCC	TCAAGTGATC	CICICACCIC	TGCCTCCCA?	SEQ ID NO 1 (3459) GIGITACCCAGGCTAGCCTCAAACCCCTGGCCCTCGGCCTCAAGTGATCCTCTCACCTCTGCCTCCCAAAGTGCTGGGTATTACAGATGTG	CAGATGTG
SEQ ID NO 13									
EQ ID NO 16	(1)								
SEQ ID NO 17	. (1)			1 1 1 1 1 1 1					
Consensus (3459)	; (3459)								

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SEQ NO 11, 13, 15, 16 and 17 against SEQ NO 1

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SEQ NO 11, 13, 15, 16 and 17 against SEQ NO 1

3913	TGAAGTCAC	4004	AGCTICACA	Section 45 4095	TTTCTAAAA
3800	O D D D D D D D D D D D D D D D D D D D	3990	SAAAICICICICA	4080	ATGAATCAA
200	DU	3980	GACACGICIG	4070	TGTTCCTAGA
	ATCTCATAGG	3970	TGGTGAGAAC	4060	TAGGAAGTGA
	H	3960	IGITGAAIIC	4050	ACAACAACII
	AAAAATCA(3950	NGATAGCCAC;	4040	ATAGCGCCAAA
	4	3940	TGTGGAAATP	4030	TCTTCTCACACACACACACACACACACACACACACACAC
	SEQ ID NO 1 (3823) TGGTGCCTATTGGAATATGCCAGGCCTCCTGTGAAAATCAGTAAGTGCTTATCTCATAGGACCAACGTTCCTGAAGTCAC EQ ID NO 11 (1)	3930	SEQ ID NO 1 (3914) TACCACACTTTGCACTTATCTCCATGTGGAAATAGCCACTGTTGAATTCTGGTGAGACGACGCTCTGAAATCTCTCACACACA	4020	SEQ ID NO 1 (4005) ACCCCTATTACAGCCCTCAGAGAATCTTCTCACATAGCGCCAAACAACAACTTTAGGAAGTGATGCTTCTAGAATGAAT
	0	3920	ACACTTIGCA	4010	CTATTACAGC
(2023) 2023	(1) (1) (1) (1) (1) (1) (3823)	(3914) 3914	(3914) TACCA (1) (1) (1) (1) (3914)	(4005) 4005 4010	(4005) ACCCCTATT (1) (1) (1) (1) (1)
	SEQ ID NO 1 (3823) SEQ ID NO 11 (1) SEQ ID NO 13 (1) SEQ ID NO 15 (1) SEQ ID NO 16 (1) Consensus (3823)		SEQ ID NO 1 (3914) SEQ ID NO 11 (1) SEQ ID NO 13 (1) SEQ ID NO 15 (1) SEQ ID NO 16 (1) SEQ ID NO 17 (1) Consensus (3914)		SEQ ID NO 1 (4005) SEQ ID NO 11 (1) SEQ ID NO 13 (1) SEQ ID NO 15 (1) SEQ ID NO 16 (1) SEQ ID NO 17 (1)

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SEQ NO 11, 13, 15, 16 and 17 against SEQ NO 1

(4086) 4096 4010 4110 4120 4130 4140 4150 4160 4170 4160 1170 4180 4170 (4086) 1170 4180 4170 4180 4170 4180 4170 (1)										Section 46
SEO ID NO (4096) TIAAAAGTGAAAACATGACAAGGGAGGGTCAGAAAGGCTGATGTTACTAAAAGACAAAAGACACTTTATG SEO ID NO (1)		(4096) 4096	4110		4130	4140	4150	4160	4170	4186
(1) Section (1) Se	SEQ ID NO 1	(4096) TTAAAAGTG	AAAACAATGAC 	3AAGGAGAAGG	GAGGGTCAG!	AGAGGAAAGGC	TGATGTTAC1	TAAAAGACAA. 	AAGACAGTATA!	ACCICITAIGA
(4096) (4096) (4187) 4220 4220 4230 4240 4250 4260 (4187) GGATGGTCCAGACAATGCAGGAAATAAAGATAAGATTGGAGGTTTGACCACTGTGATGCTTATGTGTGGACC (1)	SEQ ID NO 13 SEQ ID NO 15 SEQ ID NO 16	EEES								
(4187) 4187 4200 4210 4220 4230 4240 4250 4260 CONTRIBUTED CONTRIB	SEQ ID NO 17 Consensus	(1); (4096)	 		 	 				Section 47
(4187) GGAIGGICCAGACACITAIGIGAACTATAAAAGAITAAAAGAITAGAACTTIGAACCACACIGIGAIGGCTAACITIAIGIGGACCCCACIGIGAIGGCTAACTTIAIGIGAACCCACACACACTTIAIGIGAACCCACACACACACACACACACACACACACACA		(4187) 4187	4200	4210	4220	4230	4240	4250	4260	4277
(1)	SEQ ID NO 1	(4187) GGATGGTCC	AGACACTCAGG	GAAATGCAGG	SAAGAAATAAF	AAGATAGGAGI	TIGAACCACA	ACTGTGATGG	CTAACTTTATG	IGTGGACCCGA
(1)	EQ ID NO 13	(E) (E) (E) (F) (F) (F) (F) (F) (F) (F) (F) (F) (F								
(4278) 4278		ΞΞŝ								
(4278) 4278 4390 4310 4320 4330 4340 4350 (4278) CCGATCTATGTAAAGCACTATTTCTGGGTGCGTCAGTGAGGGTGTTTTTGGAAGAGACACTTGAAGT (1)	Consensus	(1); (4187)	1 							
(4278) CCGATCTATGGGACACCCAGATAGCTTGTAAAGCACTATTTCTGGGTGCGTCAGTGAGGGTGTTTTTGGAAGAGATCAACACTTGAGT (1)		(4978) 4978	4290	4300	4340	4920	7930	7340	4350	Section 48
(1)	SEQ ID NO 1	(4278) CCGATCIAT	GGGACACCCAG	SATAGCITGIA	AAAGCACTATI	TTCTGGGTGCG	TCAGTGAGGG	TYTE STEEL	AAGAGATCAACA	ACTIGAGICAG
SEQ ID NO 15 (1)	SEQ ID NO 11	(1)		1						
JEQ ID NO 16 (1)	EQ ID NO 15	(1)								
SEQ ID NO 17 (1)	SEQ ID NO 16	(1)								
	Consensus	(4278)	 		1	 				

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SEQ NO 11, 13, 15, 16 and 17 against SEQ NO 1

SEQ ID NO 1 (4369) 4369 4389 4380 4440 4410 4420 4430 4440 4440 4459 SEQ ID NO 1 (4369) TAGACTGAGTAAAGCAGATGGTCCTCACCAATGTGGGTGCACATTGTTTAATCTGTTGAGTGCCTGGATAGACAAAAAGGCAAAAGAAGGCAAAAGAGAAGGCAAAAGAAG
Consensus (456) 4551 4560 4570 4570 467

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SEQ NO 11, 13, 15, 16 and 17 against SEQ NO 1

										Section 52
	(4642) 4642	4650	4660	4670	4680	4690	4700	4710	4720	4732
SEQ ID NO 1	1 (4642) TCAAG	CTAAAATAC	SEQ ID NO 1 (4642) TCAAGCTAAAATACACTACCAGCTT	TCCCTIGITC	CCCTTGTTCTCTAGTGTAGGGACAGCAAATCATGAAACCTTCTGCCTCCATAATCATAAGTCAA	GGACAGCAAA	TCATGAAACC	TICIGCCIC	CATAATCATA	TAAGTCAA
SEQ ID NO 11 SEQ ID NO 13	(1) (2) (3) (-1) (-1) (4) (4) (4) (4) (4) (5) (5) (6) (7) (7) (7) (7) (7) (7) (7) (7) (7) (7									
SEQ ID NO 16 SEQ ID NO 17	EEE									
Consensus (4642)	s (4642)									Section 53
	(4733) 4733	4740	4750	4760	4770	4780	4790	4800	4810	4823
SEQ ID NO 1	1 (4733) TICCC	GTAATAAAT	SEQ ID NO 1 (4733) ITCCCGTAATAAATCTGTGCTTATA	ATATCTATAGCTTTCCT	CITICCITII	TITGGICIGIIIC	TICICCAAAGAACCTTAAIGTACACACTATAIGACCTAAC	CTTAATGTA	CACACTATAT	GACCIAAC
SEQ ID NO 11 SEQ ID NO 13	(1)									
SEQ ID NO 15 SEQ ID NO 16	(1)									
SEQ ID NO 17 (1) Consensus (4733)	7 (1) s (4733)			 - - - - - -		 - - - - - -	 - - - - - -	 - - - - - -	 - - - - - -	 - - - - -
										Section 54
	(4824) 4824	4830	4840	4850	4860	4870	4880	4890	4900	4914
SEQ ID NO 1	1 (4824) CIGIA	GTAATGATA	SEQ ID NO 1 (4824) CTGTAGTAATGATAACCTTATGCAG	GGTTTGAATA	GITIGAATAAGAIGAIGGIAITCICAGIAICIGGGAGGIAIGGGCIAGAGIGAIGAACCACCGCCA	ATTCTCAGTA	TCTGGGAGGT	ATGGGCTAG	AGTGATGAAC	CACCGCCA
SEC ID NO 13	(1)									
SEQ ID NO 15	(1)									
SEQ ID NO 16	5 (1)		.							
SEQ ID NO 17	7 (1)									
Consensus (4824)	s (4824)									

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SEQ NO 11, 13, 15, 16 and 17 against SEQ NO 1

5005	GTAGAACTA	5096	GGTTATTGC	5187 ATGAAATAC
4990	SEQ ID NO 1 (4915) TGAGCCTAGGACTGTTCTGAAATGTGGAATATTTGGTGTCAAAACCAAGAGATATTTGGTGTAATATTTGGAAAACTGTAGAACTAGTAGAACTAGTGGAAAACTGTAGAACTAATATTTGTGTGTAGAACTAGTGGAAAACTGTAGAACTAATATTTGGTGTAGAACTAATATTTGGTGTAGAACTAATATTTGGTGTAGAACTAATATTTGGTGTAGAACTAATATTTGGTGTAAACTAGTAGAACTAATATTTGTAGAACTAATATTTGTAGAACTAATATTTGGTAAACTAGTAGAACTAATATTTGTAGAACTAATATTTGTAGAACTAATATTTGTAGAACTAATATTAGAACTAAACTAAACTAAACTAAACTAAACTAAACTAAAACTAAAACTAAAACTAAAACTAAAACTAAAACTAAAACTAAAACTAAAACTAAAACTAAAACTAAAACTAAAACTAAAACTAAAACTAAAACTAAAAACTAAAAACTAAAAACTAAAAACTAAAAACTAAAAAA	5080	SEQ ID NO 1 (5006) TCGTATGATTCAGCAACCACTGGGAATTTACCCAAGGAAAGGAAACCAGTATTAAAAGAGAATCTGCACTCCCATGGTTATTGC EQ ID NO 11 (1)	SEQ ID NO 1 (5097) 5097 5097 5100 5120 5130 5140 5150 5160 5170 5187 5187 5187 5187 5187 5187 5187 5187
4980	ATATAGCCAT	5070	AAAGAAATC	5160 AAAAIGIGGC
4970	CCAAGAGATA	5060	CCAGTATATT	5150 ATGGACAAAG
4960	GGTGTCAAAA	5050	GGAAAGGAAA	5140 GATTAGATGA
4950	TGGAATATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	5040	TTTACCCAAA	5130 CAACCTAGGA
4940	TTCTGAAATG	5030	CCACTGGGAA	5120 GATAIGGACT
4930	CTGAGGAGAT	5020	AGCAACCCAA	5110 CAATAGCCTA
5 4920	15) TGAGCCTAGGA (1)	(O	O I I I I I I I I I I I I I I I I I I I	CATTATICT
(4915) 4915 4920	(4915) TGZ (1) (1) (1) (1) (1) (1) (1)	(5006) 5006	(5006) TCGTAT (1) (1) (1) (1) (1) (5006)	(5097) 5097 (5097) AGC (1) (1) (1) (1) (1)
	SEQ ID NO 1 (4915) SEQ ID NO 11 (1) SEQ ID NO 13 (1) SEQ ID NO 15 (1) SEQ ID NO 16 (1) SEQ ID NO 16 (1) SEQ ID NO 17 (1) Consensus (4915)		SEQ ID NO 1 (5006) SEQ ID NO 11 (1) SEQ ID NO 13 (1) SEQ ID NO 15 (1) SEQ ID NO 16 (1) SEQ ID NO 16 (1) SEQ ID NO 17 (1) Consensus (5006)	SEQ ID NO 1 (5097) SEQ ID NO 1 (5097) SEQ ID NO 11 (1) SEQ ID NO 13 (1) SEQ ID NO 15 (1) SEQ ID NO 16 (1) SEQ ID NO 16 (1)

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SEQ NO 11, 13, 15, 16 and 17 against SEQ NO 1

5278	CGAGGCC	5369	AAATCAT	5450 5460	ICTGATT
	AAGATCTC		AAGAATA <i>X</i>	5450	CACATAT
5260	79 0 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	5350	CCTTAAAAA	5440	GTTAAACCC GTTAAAACCC GTTAAAAAAAAAAAAAAAA
5250	CTTGGGAGGC	5340	AATAGGCCTT	5430	GGAACAGCAAA
5240	ATCCCAGCTC	5330	ACAATTTAAA 	5420	AAATTAGCCA
5230	D	5320	## CT	5410	TGTTAAGTG
5220	DCOAGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGT	5310	ATAAGACTCC	5400	3AGGATATTA(
5210	ATTAGCCAAA	5300	GGGCAAAT	5390	ATGGGACTGC
5200	FATAAAAAGP	5290	74 G A G C C A G C C C A G C C C A G C C C A G C C C A G C C C A G C C C A G C C C A G C C C A G C C C A G C C C A G C C C A G C C C A G C C C A G C C C A G C C C A G C C C A G C C C C	5380	GGCAACATAG
(5188) 5188	SEQ ID NO 1 (5188) TTACCAGCTATAAAAAGAATTAGCCAAAGCAGTGGTGTGTCATCCCAGCTCCTTGGGAGGCTGAGGTGGGAAGATCTCGAGGCCGAGGCCTGAGGCCCAGCTCCTTGGGAGGCTGAGGTGCGAAGATCTCGAGGCCCGCCTATAAAAAAAA	(5279) 5279	SEQ ID NO 1 (5279) AGAAGTTTGAGACCAGGCAAAATAATAAGACTCGGTCTCTAAAAATAGGCCTTCCTT	(5370) 5370	SEQ ID NO 1 (5370) GTCATTCACGGCAACATAGATGGGACTGGTTAACTGTTAAGTGAAATTAGCCAGGAACAGCAAGTTAAACCCCACATATTCTGATT EQ ID NO 11 (1)
	SEQ ID NO 1 (5188) SEQ ID NO 11 (1) SEQ ID NO 13 (1) SEQ ID NO 15 (1) SEQ ID NO 16 (1) SEQ ID NO 17 (1) Consensus (5188)		SEQ ID NO 1 (52/9) SEQ ID NO 11 (1) SEQ ID NO 13 (1) SEQ ID NO 15 (1) SEQ ID NO 16 (1) SEQ ID NO 17 (1) Consensus (52/9)		SEQ ID NO 1 (5370) SEQ ID NO 11 (1) SEQ ID NO 13 (1) SEQ ID NO 15 (1) SEQ ID NO 16 (1) SEQ ID NO 17 (1) Consensus (5370)

SEQ NO 11, 13, 15, 16 and 17 against SEQ NO 1

(5461) 5461 5470 5480 5500 5510 5520 5530 5540 (5461) CATATGCGGAAGGTTGATCTCATAGAAGTAAAAGTAGAAGAGGATGTTGGAGACTAGAAAAGGAAGG										*	Section 61
(1)		(5461) 5461	5470	5480	5490	5500	5510	5520	5530	5540	5551
(1)	NO 1	(5461) CATAT	GCGGAAGCTA	AAAAACGIIC	SATCICATAG	AAGTAAAAAG	TAGAACAGAG	GATGCTGGAG	ACTAGAAAA	GGTAGGGAGA	AGGAAGG
(1)	NO 13 13 13		 								
(1)	NO 15	(1)									
(1) Section (562) 5552 5560 5570 5580 5690 5610 5620 5630 5630 (1) Section (562) 5552 5560 5570 5580 5690 5610 5620 5630 5630 (1) Section	NO 16	(1)				 	 				
Section Sect	NO 17	(1)									
(15.2) GAGGGAAAATITGITAACAGGTACAAAATTACAGTTAGTTAGGGAATTAATTCCAGCATCCTGTAGGATTAAGGATTAATTCCAGCATCCTGTAGGATTAAGGATTAATTCCAGCATCCTGTAGGATTAAGGATTAATTCCAGCATCCTGTAGGATTAAGGATTAATTCCAGCATCCTGTAGGATTAAGGATTAATTCCAGCATCCTGTAGGATTAAGGATTAATTA		(1010)									Section 62
(552) GAGAGGAAAAATTIGTTAACAGGTACAAAATTACAGTTAGTTAGGGAGAATTAATT		(5552) 5552	5560	5570	5580	5590	2600	5610	5620		5642
(1)	NO 1	(5552) GAGAG	GGAAAAATTI	GTTAACAGGTA	ACAAAAACAA	AATTACAGTT	AGTTAGGGAG	AATTAATTCC	AGCATCCTG	TAGCACTATA	SGATGAC
(1)	N C C										
(1)	NO 15	(1)									
(1)	NO 16	(1)									
Section Sect	NO 17	(1)	 	 			 				 - - - -
(5643) 5643 5650 5660 5670 5720 5720 (5643) TATAGTTAATAATAATAGTCTCCAAATAGCTAGAAGGAGGATATTGAATGTTCCCAACACACAC	2	(2000)									Section 63
(5643) TATAGTTAATAATAATACTTTAATT (1)		(5643) 5643	5650	5660	5670	5680	5690	5700	5710		5733
	D NO 1	(5643) TATAG	TTAATAATAA	TACTITAATI	AGTCTCAAAT	AGCTAGAAGG	AGGATATTGA	ATGTTCCCAA	CACACACAA	AAAATGATA.	ATGTATG
7 7 7	NO 11	(1)									
NO 15 (1)	NO 13					1 1 1 1 1 1 1 1					
NO 16 (1)	NO 15	(1)			 						
NO 17 (1)	NO 16	(1)									
	NO 17	(1)									
	o loudo	(56/3)									

SEQ NO 11, 13, 15, 16 and 17 against SEQ NO 1

Section 64	5824	GATCIGATCACTTTATATGTATCAACACATCACTATGTACCCCCACAAATATGTAGAATTTT	Section 65 5915	SEQ ID NO 1 (5825) TATTIGICCATITAAAAAAGAIAACCAAATITAAAAATAAAAATAAAAT	Section 66	TGTTCCACTGCTCACTGGAACTTCCCTAGTCAGGTTGGGC
	5810	CCACACAAATA	2900	TGGATGAAC	5990	ACTTCCTAG
	5800	ACTATGTACC	5890	CATGTAAACC	CRO?	CTCACTGGAA
	5790	CAACACATC	5880	ATTAGTGTTC TTAGTGTTTC	5970	GTTCCACTG
	5780	ATTATATGTA	5870	[AAAAACTAA]	5980	A G T
	5770	TCACTCTAC	5860	AAAATAAAA1	5950	CCCAAGGCTCCAAGGCTCCAAGGCTTCAAGGCTTCCAAGGCTTCCAAGGCTTCCAAGGCTTCCAAGGCTTCCAAGGCTTCCAAGGCTTCCAAGGCTTCCAAGGCTTCCAAGGCTTCCAAGGCTT
	5760	CCTGATCTGA	5850	AACAAAIIIA 	5940	GTCAAAGITT
	5750	SEQ ID NO 1 (5734) AGATGATGGATATGGTAGTTATCCT EQ ID NO 11 (1)	5840	TAAAAAAGAT	5930	H H H H
	5740	34) AGATGATGGATA (1) (1) (1) (1) (1) (1)	5830	TIGICCAIT		CIGCCCATC
	(5734) 5734	(5734) AGA (1) (1) (1) (1) (1) (1) (1)	(5825) 5825 5830	(5825) TATT (1) (1) (1) (1) (1) (5825)	(5916) 5916	(1)
		SEQ ID NO 1 (5734) SEQ ID NO 11 (1) SEQ ID NO 13 (1) SEQ ID NO 15 (1) SEQ ID NO 16 (1) SEQ ID NO 17 (1) Consensus (5734)		SEQ ID NO 1 (5825) SEQ ID NO 11 (1) SEQ ID NO 13 (1) SEQ ID NO 15 (1) SEQ ID NO 16 (1) SEQ ID NO 17 (1) Consensus (5825)		SEQ ID NO 11 SEQ ID NO 11 SEQ ID NO 13 SEQ ID NO 13 SEQ ID NO 15 SEQ ID NO 16

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SEQ NO 11, 13, 15, 16 and 17 against SEQ NO 1

									Section 67
	(6007) 6007	6020	6030	6040	6050	6060	0209	9080	2609
O ID NO 1	(60	ATTTACAGCAA	TAGIGAAIII	ATCACIGACA	TITCITCAGI	TCCCCTCTT	GGCATCIGC	ATTTAICACTGACATITCTTCAGTTCCCCTCTTTGGCATCTGCTTCTTTTTTTTGTAATGCTGTT	TAATGCTGTT
SEQ ID NO 13 SEQ ID NO 13 SEQ ID NO 15 SEO ID NO 15									
SEQ ID NO 17 (1) Consensus (6007)	(1) (6007)								
	8609 (8609)	6110	6120	6130	6140	6150	6160	6170	Section 68 6188
O ID NO 1	(0)	TGCCCAACAII	CITITICITC	CCIAGAGCIA	TICAGGGIGA	CCTITCITII	CGCATITIC	TCCCATGCCACTTCCATTATATCAA	ATTATATCAA
SEQ ID NO 11 SEQ ID NO 13	(1) (2) (1) (2) (3) (4) (4) (5) (7) (7) (7) (7) (7) (7) (7) (7) (7) (7								
SEQ ID NO 16	(1)								
SEQ ID NO 17 (1) Consensus (6098)	(1) (6098)								
	(6189) 6189	8200	6210	8220	6230	6240	6250	8280	Section 69
O ID NO 1	(618	AGICCIGIGIG	GCCACIGCIC	AIGACCIIGI	TICCIGCCAT	GTGAAGATAG	GATCGGCTG	GCTCATGACCTTGTTTCCTGCCATGTGAAGATAGGATCGGCTGCTGTTTTTTTT	TCCTTTTTT
SEQ ID NO 11	(1)								
SEQ ID NO 15	(1)			1 1 1 1 1 1 1 1 1 1					
) ID NO 16	(1)								
SEQ ID NO 17	(1)								
Consensus (6189)	(6189)								

SEQ NO 11, 13, 15, 16 and 17 against SEQ NO 1

CICTCCCTGTCACCCAGACTGGAGTGCAATGGCACAGTCGTGGCGCCTCGAACTCCTGGACCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCT	CCCAGACTGGAATGGCACAGTCGTAGCTTGCTGCAACTCCTGGACCTCCTC 6400 6410 6420 6430 6440 6450 GCACACCACCATGCTTCTAATTTATATATATATATATATA	6290	6300	6310	6320	6330	6340	6350	6360	Section 70 6370
6400 6410 6420 6430 6440 6450 GCACACCACCATGCTICCTAATCTGATATATATATATATATATATATATATATATA	6400 6410 6420 6430 6440 6450 GCACCACCATGCCTTCCTAATCTGATATATATATATATAT	A T (TCTCCCTGTCACC	CAGACIGGA	AGTGCAATGG(CACAGICGIAG	CTTGCTGCAG	SCCTCGAACT	CCTGGACCTC	CTCAGC
6400 6410 6420 6430 6440 6450 GCACACCACCATGCCTTCCTAATCTGATATATATATATAT	6400 6410 6420 6430 6440 6450 GCACACCACCATGCCTTCCTAATCTGATATATATATATAT									
GCACCACCATGCCTTCCTAATCTGATATATATATATATAT	6400 6410 6420 6430 6440 6450	i								
GCACCCCATGCCTTCCTAATCTGATATATATATATATATA	GASOC CACCATGCCTTCCTAATCTGATATATATATATATATATAT	80	6390	6400	6410	6420	6430	6440		6461
Section 6490 6500 6510 6520 6530 6540 TATATATATATATATATATATATATATATATATATATA	6490 6500 6510 6520 6530 6540 TATATATATATATATATATATATATATATATATATATA		666ACTACA6616C	ACACACACACACACACACACACACACACACACACACAC		AAICIGAIAIA 1	TATATATATATATA	ATAITAITAIA 	TATATAAAA	
6490 6500 6510 6520 6530 6540 TATATATATATATATATATATATATATATATATATATA	6490 6520 6520 6520 6540 TATATATATATATATATATATATATATATATATATATA									Section 72
TATATAATATATATATATT 	TATATATATATATATATTT	0	6480	6490	6500	6510	6520	6530		6552
		ATA	.TTTATATATTATA	ATATATATA 	ATATATATTT	FATATATAAAA 	TATATATATT 	[ATATATATA] 	TATTATATAI 	FAAAATA
				1 1 1 1 1 1 1 1 1 1	 	 			 	

SEQ NO 11, 13, 15, 16 and 17 against SEQ NO 1

										Section 73
	(6553) 6553	6560	6570	6580	6590	0099	6610	6620	0630	6643
SEQ ID NO 1	(6553) TATAT	ATTATATAT 	SEQ ID NO 1 (6553) TATATATATATATATATATATA EQ ID NO 11 (1)	[⊢]	TATAGAGATGGGGTCTTGCTCTGTCACCCAGGCTGAAGATCAGCTGCTCTTTCTAATCTGTGGTT	GCTCTGTCAC	CCAGGCTGAA	GATCAGCTG	CICITICIAAI	CIGIGGII
SEQ ID NO 13 SEQ ID NO 15										
SEQ ID NO 17 (1) Consensus (6553)	(1) (1) (6553)									
										- Section 74
	(6644) 6644	6650	0999	6670	0899	0699	6700	6710	6720	6734
SEQ ID NO 11	(1)		SEQ ID NO 1 (0044) AGA LAAGA ICTG LCTCCAGGGGA I. SEQ ID NO 11 (1)	1 A A A A I A C I 	AAAAIACIACCIGGAAIAAAGGIAICIIIAAAAIAAICCCAGAGAAGAAACAIII 	AAGGIAI(II 	1AAA1AA1C 	CCAGAGAAG. 	⊣	1A1AG1A1G
SEQ ID NO 15	(E)									
SEQ ID NO 16 SEQ ID NO 17	(1)									
Consensus (6644)	(6644)									Section 75
	(6735) 6735 6740	6740	6750	6760	6770	6780	6790	0890	6810	6825
SEQ ID NO 1	(6735) ACAGA	GGCAGAGAA	< 4	[ATTTGTTAA	TITGITAAGGCAGGACITICACCACTCCCAGTACAATCATCTGTTGTTACCTGCATACCTTACAC	TCACCACICC	CAGTACAATC	ATCTGTCTG	TTACCTGCATA	CCTTACAC
SEC ID NO 13	(1)									
SEQ ID NO 15	(1)									
SEQ ID NO 16	(1)									
SEQ ID NO 17	(1)									
Consensus (6735)	(6735)									

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SEQ NO 11, 13, 15, 16 and 17 against SEQ NO 1

(826) GGCTGGCACTGCTGGGGGTACAAGTAGATGCTAAGTTCAATGGTTAGATTCATGTTTAAAAAGCCATTGGATCAAACTTTGT (1)										Section 76
(826) (827) (827) (827) (827) (827) (837) (837) (837) (837) (837) (837) (837) (837) (837) (837) (837) (837) (837) (837) (837) (837) (838)	:	(6826) 6826	6840	6850	6860	6870	6880	6890	0069	6916
(8917) 6917 6930 6940 6950 6950 6970 6980 6990 6990 (6917) 6917 6917 6917 6917 6917 6917 6917 6917	SEQ ID NO 11 SEQ ID NO 11 SEQ ID NO 13 SEQ ID NO 15 SEQ ID NO 15	(4826) GGGCTGGC (1)	A. C. T. G.	TACAAAGTAG.	ATGCCAAACT:	ICACAATGGT	TAGATTCATG	TTTAAAAAGC 	CATIGGATCAAA	CCTTTGTGAA
(6917) 6917 6980 6990 6990 (6917) AGITICCAGCITATITCTGTTCCAAATAGTCCATAAAAGAATCTCCAAGAGTCTATGTCCATGAGT (1)	SEQ ID NO 17 Consensus	(1)								Section 77
(9917) AGTITCCAGCITITITCTGTTCCAAATAGGAATCTCAAGAGCATAATTGCCAAGATAGTCTATGTCCATGAGT (1)		(6917) 6917	0869	6940		0969	0269	0869	0669	7007
ACATCICICATGAAAICIGTICCCAICATTACICAAGAIAITGIAIGAACAGIAITCCACATAAACIAGGIGCICAAIAAIGAIT	SEQ ID NO 13 SEQ ID NO 15 SEQ ID NO 16 SEQ ID NO 17 Consensus	(1) (1) (1) (1) (6917)								Ocetics 78
(1)		(7008) 7008	7020	7030	7040	7050	7060	7070	7080	7098
207	EQ ID NO 1	(7008) TCAACATC	TCTCATGAAAT(CTGTTCCCAT	CATTACTCAA(SATATIGIAI(SAACAGTATT	CCACATAAAC 	TAGGTGCTCAAT	AATGATTGAT
(1) (7008)	2 ID NO 13									
JID NO 17 (1)	3 ID NO 16	Ξ	: 				-			
	Consensus	(7008)								

SEQ NO 11, 13, 15, 16 and 17 against SEQ NO 1

SEQ NO 11, 13, 15, 16 and 17 against SEQ NO 1

Section 82	(7372) 7372 7380 7400 7410 7420 7430 7430 7450 7450 7460 7460 7460 7460 7460 7460 7460 746		7530 7540 7553
1	7430 CAAGATTTCTC1		7520
	7420 ATTCTATAAAG		7510
5	7410 FGAACAAAAGI		7500
	7400 3TACATICATTI		7490
	80 7390 ATACTAAAAATG		7480
	(7372) 7372 7380 (7372) AATTTTCGAATA (1)	(1) (1)	(7463) 7463 7470
	(73) SEQ ID NO 1 (73) SEO ID NO 11	SEQ ID NO 13 (1) SEQ ID NO 15 (1) SEQ ID NO 16 (1) SEQ ID NO 17 (1) Consensus (7372)	(74)

SEQ NO 11, 13, 15, 16 and 17 against SEQ NO 1

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SEQ NO 11, 13, 15, 16 and 17 against SEQ NO 1

8008	NACCCTAAT	8099	NATTAAAGC	8190	ATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTC
	T G A T T F		T C T D T T C T D T T T T T T T T T T T	8180	H
7990	2AATTTCAAA	8080	LATICCIGCI	8170	DE
7980	GCATATIGGC	8070	AATCAGGTAT	8160	ACCCCTAAAC
7970	FAAATGAGT	8060	TTACATACAA	8150	CAAGTTCAGG
7960	TTTTATAGG	8050	CATATGCTG.	8140	GGTATGAAC(
7950	TGCAAAATTACAGTTTTTATAGGTAAAATGAGTGCATATTGGCAATTTCAAATGATTAACCCTAAT	8040	ATTCAGATCTTAAACATATGCTTACATACAAATCAGGTATATTCCTGCTTCTATAATTAAAGC	8130	TCTGACATGACATGA
7940	GAACCATGCA	8030	AGAATATTO TO CARA TATTO TATTO	8120	CACTACTCCT
7930	CTATTAGTTT 	8020	H H H H H H H H H H H H H H H H H H H	8110	H
(7918) 7918	SEQ ID NO 1 (7918) TCTTCATATCTATTAGTTTGAACCA EQ ID NO 11 (1)	6008 (6008)	SEQ ID NO 1 (8009) ACAITAIGCITIIGGGIAIAGAAAI. EQ ID NO 11 (1)	(8100) 8100	SEQ ID NO 1 (8100) AAAGAGAATITCTTTTGGTCACTACTCCTTCTGACATGAACCAAGTTCAGGACCCCTAAAGGTCTGGGTCTGGGTCTTCTCTCCTCCTCCTCCTCTCTCTCTCTCTCTCTCTCT
	SEQ ID NO 1 (7918) SEQ ID NO 11 (1) SEQ ID NO 13 (1) SEQ ID NO 15 (1) SEQ ID NO 16 (1) SEQ ID NO 17 (1) Consensus (7918)		SEQ ID NO 1 (8009) SEQ ID NO 11 (1) SEQ ID NO 13 (1) SEQ ID NO 15 (1) SEQ ID NO 16 (1) SEQ ID NO 17 (1) Consensus (8009)		SEQ ID NO 1 (8100) SEQ ID NO 11 (1) SEQ ID NO 13 (1) SEQ ID NO 15 (1) SEQ ID NO 16 (1) SEQ ID NO 17 (1) Consensus (8100)

SEQ NO 11, 13, 15, 16 and 17 against SEQ NO 1

	(8191) 8191	8200	8210	8220	8230	8240	8250	8260	8270	Section 91 8281
SEQ ID NO 1	1 (8191) ACCIC	TAACTIGIG	SEQ ID NO 1 (8191) ACCTCTAACTTGTGCCGCTTTCTTG	GTCAGTCAT	GICAGICATIGIGITCIGAGCIGICICATAAAACAICIGCIAIGACTITACTIT	CTGTCTCAT!	AAACAICIG(CIAIGACIII.	ACTITCICC:	IGATAGGG
SEQ ID NO 13 (1) SEQ ID NO 15 (1) SEQ ID NO 16 (1) SEQ ID NO 17 (1) Consensus (8191)	(1) (1) (2) (3) (4) (4) (4) (4) (5) (7) (7) (7) (7) (7) (7) (7) (7) (7) (7									
										Section 92
	(8282) 8282	8290	(8282) 8282 8290 8300	8310	8320	8330	8340	8350	8360	8372
SEQ ID NO 11 SEQ ID NO 13 SEQ ID NO 15 SEQ ID NO 16 SEQ ID NO 16	(1) (1) (2) (1) (1) (2) (3) (4) (4) (4) (4) (5) (7) (7) (7) (7) (7) (7) (7) (7) (7) (7									
Colliserisus (6262)	(9595)									Section 93
	(8373) 8373	8380	8390	8400	8410	8420	8430	8440	8450	8463
SEQ ID NO 1	1 (8373) CCIGCIGC	TECTCTCCC	SEQ ID NO 1 (8373) CCTGCTGCTCTCCCACATTCCCAT.	CITICICCI	CITTCICCIGAICICCICICACCIGIACAITICITACAITITCICCIGIGCTICCTICITCCCAICA	ACCIGTACATI	TCTTACATT	ITCICCIGIG	CIICCIICI	ICCCAIC
SEQ ID NO 15	5 (1)									
SEC ID NO 16	(i) 7 (i)7								 	
Consensus (8373)	s (8373)	 	 	 	 	 	 	 	 	

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SEQ NO 11, 13, 15, 16 and 17 against SEQ NO 1

8554	FTTCCTTCTG	8645	Section 96	8736	CTGAGCTTCT
8540	CC C C C C C C C C C C C C C C C C C C	8630		8720	3GTGATCAAA(
8530	TGCAGAGATO	8620		8710	CCAAACTAGC
8520	CTCTCACATA	8610		8700	TCAGCTCAGG
8510	CICCTIGICACATITICCTITIGCCGGCTCTCACATAIGCAGAGATGGCTCTIGGITITICCTICIG	0 8590 8600 8610 8620 8630 8645		8690	CAAAGAACTCACTGTTTCAGTGCTTTCAGCTCAGGCCAAACTAGGGTGATCAAACTGAGCTTCT
8500	TGTCACATTI	8590		8680	AACTCACTGT
8490				8670	
8480	SEQ ID NO 1 (8464) TCATTGCCCAAGTGTGTCTTCTTTCTTGEQ ID NO 11 (1)	8555) 8555 8560 8570 858		3660	SEQ ID NO 1 (8646) CATITICCTGGTTTCTAGAAGTAAGACC EQ ID NO 11 (1)
8470	TGCCCAAG	8560			H L C C L G G B L L L L L L L L L L L L L L L L
(8464) 8464	(8464) TCAT (1) (1) (1) (1) (1) (1)	(8555) 8555 8560	(1) (1) (1) (1) (1) (1)	(8646) 8646	(1) (1) (1) (1) (1)
	SEQ ID NO 1 (8464) SEQ ID NO 11 (1) SEQ ID NO 13 (1) SEQ ID NO 15 (1) SEQ ID NO 16 (1) SEQ ID NO 17 (1) Consensus (8464)		SEQ ID NO 11 (1) SEQ ID NO 13 (1) SEQ ID NO 15 (1) SEQ ID NO 16 (1) SEQ ID NO 17 (1) Consensus (8555)		SEQ ID NO 11 SEQ ID NO 11 SEQ ID NO 13 SEQ ID NO 15 SEQ ID NO 16 SEQ ID NO 17

SEQ NO 11, 13, 15, 16 and 17 against SEQ NO 1

Section 97 8827 GGTCACTAATT	8918 TATICIGGGIG	Section 99 0009 046604T0AT0 04660AT0AT0
Section 97 S770 S780 S780 S810 S827 S	8880 8890 8900 8918 AATTTAIGCATCAACCIGGCTAAAGGATGACCAGGTAGCTGGTAAAACATTATICIGGGTG	8950 8950 8950 8990 9009 GATCAGCATITGAATITGGTAAAGCAGACGGCTCTCACCAATAAGGGCAGGCATCATC 8990 9009 ATTTGAATTGGTGAACTTAGTAAAGCAGGCTCTCACCAATAAGGGCAGGCA
8800 AAATACCAT?	8890 3ACCAGGTAGC	8980 GACGGCTCTC IGACGGCTCTC IGACGGCTCTC IGACGGCTCTC
8790 CITCACTGT1	8880 SCIAAAGGAIG	8970 TAGTAAAGCA TAGTAAAGCA
8780 ATCTACAAAT	8870 CCTGGCTAGG	8960 TTGGTGAACT TTGGTGAACT
8770 TAGACAGACC	8860 TATGCATCAA	8950 AGCATTEAA ATTTEAA
8760 TAAAACCAAG	8850 TAATTAAATT	8940 GGAAGATC
8750 TCAAAACCIA 	8840 ATAIGIGIGA 	8930 GAGIGITITC
SEQ ID NO 1 (8737) 8737 8750 876 SEQ ID NO 1 (1)	(8828) (SEQ ID NO 1 (8919) 8919 8930 8930 8940 SEQ ID NO 1 (8919) TGTCCATAAGAGTGTTTTCGGAAGA SEQ ID NO 11 (1)

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SEQ NO 11, 13, 15, 16 and 17 against SEQ NO 1

9100	TCTCCTGCCCTT TCTCCTGCCCTT TCTCCTGCCCTT TCTCCTGCCCTT TCTCTGCCCTT TCTCTGCCTT TCTCTGCCCTT	9191	ACACTGC ACACTGC CACTGC	TACACTGC Section 102	9282 ATTTACAT ATTTACAT
0606	ATCITCTCC ATCITCTCC ATCITCTCC ATCITCTCC	9180	GACTGAATT	GACTGAATI	9270 TCCATITIA TCCATITIA
9080	TAGIAIATO TAGIAIATO TAGIAIATO	9170	1100ACTTG 1200ACTTG 1200ACTTG	TIGGACIIG	9260 GAGTCAATT GAGTCAATT
9070		9160	CCAGGAGITACACCITIGGCITCCCIGGITCTCAGITCTITGGACTIGAATTACACIGC CCAGGAGITACACCITIGGCITCCCIGGITCTCAGITCTITGGACTIGGACTGAATTACACIGC CCAGGAGITACACCTTIGGCITCCCTGGITCTCAGITCTITGGACTTGGACTGAATTACACTGC	CCAGGAGTTACACCTTTGGCTTCCCTGGTTCTCGGACTTGGACTGGACTGAATTACACTGC Section 102	9220 9230 9250 9260 9270 9282 SATGGGAGATOATGGGACTTGTTGGCGTCCATAATTGTGTGAGTCAATTTCCATTTTATTTA
0906	TGCTTCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	9150	HOUSE	CIICCCIGGI	9240 9250 TOTTGGCCTCCATAATTGTTTGGCCTCCATAATTGTTTGGCCTCCATAATTGTTTGGCTTCATAATTGTTTTTTTT
9050	AAAAGAGGAAGGGAAATTTGCTTCTTT AAAAGAGGAAGGGAAAITTGCTTCTTTT AAAAGAGGAAAAITTGCTTCTTTT 	9140	ACACCTTTGG ACACCTTTGG ACACCTTTGG	ACACCITIGE	9220 1060A6A10A1666ACTT 1060A6A10A1666ACTT 1000A6A10A1666ACTT 1100A6A10A1666ACTT 1100A6A10A1666ACTT 1100A6A10A1666ACTT 1100A6A10A1666ACTT
9040		9130	AACCAGGAGTT AACCAGGAGTT AACCAGGAGTT AACCAGGAGTT		9192 9200 9220 9230 9240 9250 9192 0402 9220 9230 9240 9250 9192 0402 0402 0402 0402 0402 0402 9192 0402
9030	010) CAATCTGTCGAAAGCTTGAATAAACA (60) CAATCTGTCGAAAGCTTGAATAAAACA (10) CAATCTGTCGAAAGCTTGAATAAAACA (1)	9120	9101) GGATGTGAGTGGGCCTTCAGACTTAAA (151) GGATGTGAGTGTAAA (151) GGATGTGAGTGGGGCCTTCAGACTTAAA (151) GGATGTGAGTGGGGCCTTCAGAGTGGGGGGGGGGGGGGG	TCAGACTTAA	9192) 9192 9210 9192) CAGGTTTCCTGGTTCTCCAGCTTGCAG (242) CAGGTTTCCTGGTTCTCCAGCTTGCAG (1)
0 9020	GTCGAAAGCT GTCGAAAGCT GTCGAAAGCT 	9110	6A6T666CCT	GAGTGGGCCT	9200
(9010) 9010	SEQ ID NO 1 (9010) CARTCTGTCGAAGCTTGAATAAACA EQ ID NO 11 (60) CAATCTGTCGAAGCTTGAATAAACA EQ ID NO 13 (60) CAATCTGTCGAAAGCTTGAATAAACA EQ ID NO 15 (1)	(9101) 9101	SEQ ID NO 1 (9101) SGATGTGAGTGGGCCTTCAGACTTAAA EQ ID NO 11 (151) GGATGTGAGTGGGCCTTCAGACTTAAA EQ ID NO 13 (151) GGATGTGAGTGGCCCTTCAGACTTAAA EQ ID NO 15 (1)	Consensus (9101) GGAIGIGAGIGGGCCTICAGACTIAAA	9210 9210
	SEQ ID NO 11 SEQ ID NO 11 SEQ ID NO 13 SEQ ID NO 15 SEQ ID NO 15 SEQ ID NO 16 SEQ ID NO 16 Consensus		SEQ ID NO 11 SEQ ID NO 11 SEQ ID NO 13 SEQ ID NO 15 SEQ ID NO 16 SEQ ID NO 16	Consensus	SEQ ID NO 1 (SEQ ID NO 11 SEQ ID NO 13 SEQ ID NO 13 SEQ ID NO 15 SEQ ID NO 16 SEQ ID NO 16 SEQ ID NO 17 Consensus (

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SEQ NO 11, 13, 15, 16 and 17 against SEQ NO 1

Section 103	9373	GAGTGTAA GAGTGTAA 	9464	CATGATA CATGATA	Section 105 9555	CAATCCT
	9360	SEQ ID NO 1 (9283) ATCCAGTTATGCATTGCTTAACAATGGAGACAGGTTCTGAGAAATGCATTGTTAAGTGATTTCATCATTGTGCAAACATCATAGGAGTGTAA SEQ ID NO 11 (333) ATCCAGTTATGCTTAACAATGGAGACAGGTTCTGAGAAATGCATTGTTAAGTGATTTCATCATTGTGCAAACATCATAGGAGTGTAAA SEQ ID NO 13 (306)	9450	SEQ ID NO 1 (9374) CTACACAAACCTGGACAGCATACTACACATCTAGGCTACATGGTGTAGCTTGTAACCTCATGATAAGTATGTAT	05.40	9465) AGTATGTATCTACCATATCTAAATGTAGAAAAGGTACAGTAAAATATGGTATAATCTTATGGGATCACCATCATATATGCAATCCT (515) AGTATGTATGTATCTACCATATCTAAATGTAGAAAAGGTACAAAATTATGGTATAATCTTATGGGATCACCATCATATTGCAATCCT (306)
	9350	ATCATTGTG ATCATTGT	9440	CATGATAAG	0530	ATGGGATCA ATGGGATCA
	9340	AAGTGATTTC AAGTGATTTC 	9430	CTTGTAACCT CTTGTAACCT	0520	GTATAATCTT GTATAATCTT
	9330	ATGCATTGTT ATGCATTGTT	9420	CATGGTGTAG	0510	[AAAAATATG [AAAAATATG
	9320	TTCTGAGAAA TTCTGAGAAA 	9410	TCTAGGCTA(ดรูบบ	AAGGTACAG:
	9310	ATGGAGACAGGATGGGATGGGGGGGGGGGGGGGGGGGGG	9400	ACTACTACACA ACTACTACACA ACTACTACACA ACTACTACACA ACTACTACACA	0000	FAATGTAGAA
	9300	SEQ ID NO 1 (9283) ATCCAGTTATGCATTGCTTAACAAT EQ ID NO 11 (333) ATCCAGTTATGCATTGCTTAACAAT EQ ID NO 13 (306)	9390	ACAGCATAGF ACAGCATAGF 	0480	SEQ ID NO 1 (9465) AGTATGTATGTATCTACCATATCTA EQ ID NO 11 (515) AGTATGTATGTATCTACCATATCTA EQ ID NO 13 (306)
	9290	AGTTATGCAT AGTTATGCAT 	9380	ACAAACCTGG ACAAACCTGG 	9470	IGTATGTATC IGTATC IGTATGTATC IGTATC IGTATC IGTATC IGTATC IGTATC IGTATC IGTATC
	(9283) 9283	(9283) ATCC: (333) ATCC: (306) (1) (1) (1)	(9374) 9374	(9374) CTAC (424) CTAC (306) (1) (1) (1)	(9465) 9465 9470	
		SEQ ID NO 1 (9283) SEQ ID NO 11 (333) SEQ ID NO 13 (306) SEQ ID NO 15 (1) SEQ ID NO 16 (1) SEQ ID NO 17 (1) Consensus (9283)		SEQ ID NO 1 (9374) SEQ ID NO 11 (424) SEQ ID NO 13 (306) SEQ ID NO 15 (1) SEQ ID NO 16 (1) SEQ ID NO 17 (1) Consensus (9374)		SEQ ID NO 1 (9465) SEQ ID NO 11 (515) SEQ ID NO 13 (306) SEQ ID NO 15 (1) SEQ ID NO 16 (1) SEQ ID NO 17 (1) Consensus (9465)

SEQ NO 11, 13, 15, 16 and 17 against SEQ NO 1

_ Section 106	Section 107 9737 GCATAGGT GCATAGGT	9828 AAGAGCIC AAGAGCIC
S80 9610 9620 9630 9646 GTGCATGACTGTATACGCACACACACACACACACACATATACTATTGGTTCTTTTTCTCTGA 9646 GTGCATGACTGTATACGCACACACACACACACACACACAC	Section 107 1 GGTGAAACATATGTGGAGATGGGGCATAGGT TGGTGAAACATATGTGGAGATGGGGCATAGGT	SEQ ID NO 1 (9738) 9738 9750 9760 9770 9780 9790 9820 98
9620 .CACAAATATA(.CACAAATATA(9710 GGTGAAACATA GGTGAAACATA	9800 CAGGGCATCA(CAGGGCATCA(
9610 ACACAACACA ACACAACACA 	9700 TITAIGGITTI TITAIGGITTI 	9790 TGGGACAAGCC TGGGACAAGCC
9600 ACGCACACAT.	9680 9690 9700 TATATTGACTCTATTTCAAAATTTATGGTTT TATATTGACTCTATTTCAAAATTTATGGTTT	9780 AGGCATCATT AGGCATCATT
9590 ATGACTGTAT ATGACTGTAT	9680 TATATTGACTC TATATTGACTC	9770 AATGGGTGGG AATGGGTGGG
9580 TGTGTAGTGC TGTGTAGTGC	0 4 4 1 1 1	9760 CCTGCTGATG
9570 IGAAAIGICAI IGAAAIGICAI	9660 AATACAATATG AATACAATATG 	9750 FGGGATAGTGT FGGGATAGTGT
SEQ ID NO 1 (9556) 9556 EQ ID NO 11 (9556) TIGIAGACTGAAATGTCATTGTGTAG EQ ID NO 13 (306)	SEQ ID NO 1 (9647) 9647 9660 9670 SEQ ID NO 1 (9647) AGAGCCCTAATACAATATGTTATACA EQ ID NO 13 (306)	(9738) 9738 (9738) GTGTGAAC (788) GTGTGAAC (306) (1) (1) (1)
SEQ ID NO 1 (9556) SEQ ID NO 11 (606) SEQ ID NO 13 (306) SEQ ID NO 15 (1) SEQ ID NO 16 (1) SEQ ID NO 16 (1)	SEQ ID NO 1 (9647) SEQ ID NO 11 (697) SEQ ID NO 13 (306) SEQ ID NO 15 (1) SEQ ID NO 16 (1) SEQ ID NO 16 (1) SEQ ID NO 17 (1)	SEQ ID NO 1 (9738) SEQ ID NO 11 (788) SEQ ID NO 13 (306) SEQ ID NO 15 (1) SEQ ID NO 16 (1) SEQ ID NO 16 (1) SEQ ID NO 17 (1)

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SEQ NO 11, 13, 15, 16 and 17 against SEQ NO 1

18629 9629 9620 9650 9650 9650 9650 9670 9680 9690 9670 9670 9680 9670
9840 AAGAGCACTITATG AAGAGCACTITATG
(9829) 9829 (879) AACZ (879) AACZ (306) (1) (1) (9920) ATAZ (970) ATAZ (970) ATAZ (970) ATAZ (1)

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SEQ NO 11, 13, 15, 16 and 17 against SEQ NO 1

441111	Section 113 0 10283	A A I I I I	10310 10320 10330 10340 10350 10360 10374 ACAGICCTGACTCTIAAGGACTCAGGIAAATACTTAGGGTATTTCATGGCCCTAGTCTTTGGGGT ACAGICCCTGACTCTTAAGGACTCAGGTAAATACTTAGGGTATTTCATGGCCCTAGTCTTTGGGGT
10180 ATTCTAAAT ATTCTAAAT	10270	ATTGAAT ATTGAAT 	10360 GGCCCTA GGCCCTA
10170 TIGGITIGA.	10260	TTAACAAAC. TTAACAAAC.	10350 GIATITCAT GGIATITCAT
10160 AAACATTTTC AAACATTTTC	10250	TACCTGTTCC TACCTGTTCC	10340 AATACTTAGG AATACTTAGG
10150 FTCCTGAAA FTCCTGAAA	10240	ATATTTTAT ATATTTTTAT 	10330 SACTCAGGTA SACTCAGGTA
10140 CAAATACTCC CAAATACTCC	10230	CAAGITIGCACAAGITIGCACACACACACACACACACACACACACACACACACACA	10320 ACTCTTAAGC ACTCTTAAGC
10130 10140 10150 10160 ITACTAGTGGTCAAATACTCTTCCCTGAAAAACATTTT ITACTAGTGGTCAAATACTCTTCCCTGAAAAACATTTT ITACTAGTGGTCAAATACTCTTCCCTGAAAAACATTTT ITACTAGTGGTCAAATACTCTTCCCTGAAAAACATTTT ITACTAGTGGTCAAATACTCTTCCCTGAAAAACATTTT ITACTAGTGTCAAATACTCTTCCCTGAAAAACATTTT ITACTAGTGTCAAATACTCTTCCTTGAAAAAAAAAATTTT ITACTAGTGTCAAATACTCTTCCTTGAAAAAAAAAATTTTTAAAAAAAA	10220	TAAATACTTT TAAATACTTT	10310 ACAGICCIG
SEQ ID NO 1(10102) 10102 10110 10120 SEQ ID NO 1(10102) TGCCATGCATCATAATTCTAAATCA SEQ ID NO 11 (1152) TGCCATGCATCATAATTCTAAATCA SEQ ID NO 13 (306)	10210	SEQ ID NO 1(10193) GGTCACCACTGAGCTTTTAAATATA SEQ ID NO 11 (1243) GGTCACCACTGAGCTTTTAAATATA SEQ ID NO 13 (306)	SEQ ID NO 1(10284) 10284 10290 10300 SEQ ID NO 1(10284) ATGATTATGGGAAACATTCGGGTAT. SEQ ID NO 11 (1334) ATGATTATGGGAAACATTCGGGTAT. SEQ ID NO 13 (306)
10110 TGCATCATAA TGCATCATAA 	10200	CCACTGAGCT	10290 TATGGGAAAC TATGGGAAAC
(10102) 10102 (10102) TGCCA (1152) TGCCA (306) (1152) (1) (1) (1) (1) (1) (1)	(10193) 10193	(1243) GGTCA (1243) GGTCA (306) (1) (1) (1)	(10284) 10284 (10284) ATGAT (1334) ATGAT (306) (1) (1) (1)
SEQ ID NO 1(10102) SEQ ID NO 11 (1152) SEQ ID NO 13 (306) SEQ ID NO 15 (1) SEQ ID NO 16 (1) SEQ ID NO 17 (1) SEQ ID NO 17 (1)		SEQ ID NO 1(10193) GGT SEQ ID NO 11 (1243) GGT SEQ ID NO 13 (306) SEQ ID NO 15 (1) SEQ ID NO 16 (1) SEQ ID NO 17 (1) SEQ ID NO 17 (1)	SEQ ID NO 1(10284) SEQ ID NO 1(10284) SEQ ID NO 11 (1334) SEQ ID NO 15 (1) SEQ ID NO 16 (1) SEQ ID NO 17 (1) Consensus(10284)

SEQ NO 11, 13, 15, 16 and 17 against SEQ NO 1

Section 115 10465 AAATTGCTTG AAATTGCTTG	10556	CTGGAATATT CTGGAATATT	10847 ITTITAAAAC ITTITAAAAAC
10450 TAAGTGAACCAA TAAGTGAACCAA	10540	TACTTGTGCTTAAAATTTTGAATAGTAAAACAGAGTGTCAACTTCATGCTGGAATATT TACTTGTGCTTAAAATTTTGAATAGTAAAACAGAGTGTCAACTTCATGCTGGAATATT	10630 AGCITICITCI CAGCITICITCI
10440 GTAGACAAAA1 GTAGACAAAA1	10530	AAACAGAGTG1 AAACAGAGTG1 	10620 ACTGAAATTAC ACTGAAATTAC
10430 CAGIGAIIGI CAGIGAIIGI 	10520	TTGAATAGTA TTGAATAGTA	10610 AAGTAACATC AAGTAACATC
10420 AATGATAACA AATGATAACA 	10510	GCTTAAAATT GCTTAAAATT 	10600 TTACAAGACT TTACAAGACT
10410 CAAAATCAAG CAAAATCAAG	10500	TTTACTTGT.	10590 IGAAGTATTT IGAAGTATTT
10400 ATCACAGATT ATCACAGATT	10490	ZACTGAGAGT:	10580 LTTAAGTACA LTTAAGTACA
10390 CTTCTTCAAA	10480	CTATGGAACCCTATGGAACCC	10570 AGACACAAT: AGACACAAT:
(10375) 10375 10380 (10375) ACCACATGTTT (1425) ACCACATGTTT (306) (1) (1) (1)	(10466) 10466	6) CITCIGICATI 6) CITCIGICATI 7)	(10557) 10557 1(10557) TTTGGCTTTTTT 1 (1607) TTTGGCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT
Section 115 10375	(10466	SEQ ID NO 1(10466) CTTCTGTCATTCTATGGAACCACTGAGAGTTTT SEQ ID NO 11 (1516) CTTCTGTCATTCTATGGAACCACTGAGAGTTTT SEQ ID NO 13 (306)	SEQ ID NO 1 (10557) 10557 10570 10580 10590 10610 10620 10620 10630 10647

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SEQ NO 11, 13, 15, 16 and 17 against SEQ NO 1

(10648) 10648 10668 10650 10670 10680 10590 10700 10710 10720 10738 SEQ ID NO 1(10648) TGGTATTTGTTATAAAACTAAAAGCAATCAAGAAAAGCATAATTATTACTGAAAAAGAAAAGAAATGTACGGA EQ ID NO 11 (1698) TGGTATTTGTTATAAAACTAAAAGCAATCAAGAAATGTACTGAAAAAGAAATGTACGGA EQ ID NO 13 (306)	10750 10760 10770 10780 10790 10800 10810 10829	GAAGGAGTTAACAAATGATCCACTCTGGGTGTTGAAAACACCCAATAAGCCTGCTTCCAGGAAGTGCCTAAGACAGAGCTGGC GAAGGAGTTAACAAATGATCCACTCTGGGTGTTGAAAACACCCAATAAGCCTGCTTCCAGGAAGTGCCTAAGACAGAGCTGGC	10860 10870 10880 10890 10900 1091 AGGAAACTGCTGGGCTACATGCCACCATCCTCAGTTGTCCAGATAGAT
SEQ ID NO 1(10648) 10648 10670 10670 SEQ ID NO 1(10648) 106717175TTATAAAACTAAAGAG SEQ ID NO 11 (1698) 1GGTATTTGTTATAAAACTAAAGAG SEQ ID NO 13 (306)		SEQ ID NO 1(10739) ATAGAGGAGGAAGGAGTTAACAAAT SEQ ID NO 11 (1789) ATAGAGGAGGAAGGAGTTAACAAAT SEQ ID NO 13 (306)	0 GCTTGCT GCTTGCT
SEQ ID NO 1(10648) 10648 SEQ ID NO 1(10648) TGGT SEQ ID NO 11 (1698) TGGT SEQ ID NO 13 (306) SEQ ID NO 15 (1) SEQ ID NO 16 (1) SEQ ID NO 17 (1)	(10739) 10739	SEQ ID NO 1(10739) ATA SEQ ID NO 11 (1789) ATA SEQ ID NO 13 (306) SEQ ID NO 15 (1) SEQ ID NO 16 (1) SEQ ID NO 17 (1) Consensus(10739)	SEQ ID NO 1(10830) TCAG SEQ ID NO 1(10830) TCAG SEQ ID NO 11 (1880) TCAG SEQ ID NO 13 (306) SEQ ID NO 15 (1) SEQ ID NO 16 (1) SEQ ID NO 17 (1)

SEQ NO 11, 13, 15, 16 and 17 against SEQ NO 1

Section 121 00 11011 ATTTATTTTT ATTTATTTTT		0 11102	CCAAGITAAG CCAAGITAAG	11193	ATGCCTGAAT ATGCCTGAAT
11000 11000 TTGTCAAATITAT TTGTCAAATITAT	 	11090	TATCTAACO	11180	CTTTGACT.
10990 AATTAACT AATTAACT 	 	11080	AGTTTAAA AGTTTAAA 	11170	GTTTGCAGGGTTTGCAGGGGGGGGGGGGGGGGGGGGGGG
SEQ ID NO 11 (19921) 10930 10930 10940 10950 10950 10950 10950 10910 11011 SEQ ID NO 11 (1971) GGAAATAATCTTTAATTATGATATGAGACACCATTCAAAGCACTATGCTAAGTCCTTTATGTGAATTAACTTTTTTTT	1 1 1 1 1 1 1 1 1 1	11070	SEQ ID NO 1(11012) CATAAATAACCCAAATATGTATACCACTATTATCCTAAAGAGGAGAAACTGAGCTCCTAAAGTTTAAAATATCTAACCCAAGTTAAG SEQ ID NO 11 (2062) CATAAATAACCCAAATATGTATACCACTATTATCCTAAAGGAGAAACTGAGCTCCTAAAGTTTAAATATCTAACCCAAGTTAAG SEQ ID NO 13 (306)	11160	SEQ ID NO 1(11103) ACTGCTAGTCACCCTAGGCTATTAACTCAGGCCAGTCTAACTCAGGTATAATAACATTATGCTACTGTTTGCAGCTTTTGACTATGCCTGAAT EQ ID NO 11 (2153) ACTGCTAGTCACCCTAGGCTATTAACTCAGGCAGTCTAACTCAGGTATAATAACATTATGCTACTGTTTGCAGCTTTTGACTATGCCTGAAT EQ ID NO 13 (306)
10970 TATGCTAAG TATGCTAAG	 	11060	AGGAGAAAC AGGAGAAAC 	11150	TATAATAAC
10960 ATTCAAAGCAC ATTCAAAGCAC	1 1 1 1 1 1 1 1	11050	TACCITAAAG TACCITAAAG	11140	CTAACTCAGG
AGCTGACACCA AGCTGACACCA	 	11040	CACTATTATCC CACTATTATCC	11130	ACTCAGGCAGI
10940 TTATGATATA TTATGATATA	; 	11030	TATGTATACC TATGTATACC	11120	AGGCTATTA/AGGCTA
10930 AATCITIAA AAICITIAA	! ! ! ! ! ! !	11020	TAACCCAAA TAACCCAAA	11110	AGTCACCCT AGTCACCCT
(10921) 10921 (10921) GGAAAT (1971) GGAAAT (306) (1)	0921)	(11012) 11012	1012) CATAAA 2062) CATAAA (306) (1) (1)	1103) 11103	1103) ACTGCT 2153) ACTGCT (306) (1) (1)
SEQ ID NO 1(10921) 10921 10930 10940 SEQ ID NO 1(10921) GGAAATAATCTTTAATTATGATATAG SEQ ID NO 11 (1971) GGAAATAATCTTTAATTATGATATAG SEQ ID NO 13 (306)	Sed ID NO 17 (1) Consensus(10921)	1)	SEQ ID NO 1(11012) CATAAATAAC SEQ ID NO 11 (2062) CATAAATAAC SEQ ID NO 13 (306) SEQ ID NO 15 (1) SEQ ID NO 16 (1) SEQ ID NO 17 (1) Consensus(11012)	(1)	SEQ ID NO 1(11103) ACTGCTAGTCACCCTAGGCTATTAAC SEQ ID NO 11 (2153) ACTGCTAGTCACCCTAGGCTATTAAC SEQ ID NO 13 (306)

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SEQ NO 11, 13, 15, 16 and 17 against SEQ NO 1

SEQ ID NO 11 (224) INTERCOLLEGATE AND CONTROLLEGATE AND CONTROLLEG	(11194) 11194 11200 11210 SEQ ID NO 1(11194) TATAACGICATGCIATCTAACTAAA	11200 CGTCATGC1	11210 TATCTAACTA	11220 AAAAGCTAAG	11230 GGAAATAAAA	11240 TGAGCCATAG	11220 11230 11240 11250 11250 11260 11270 11284 AAGCTAAGGGAAATAAAATGAGCCATAGGGCTCAATTTCATAAAAGGAGAGAAAATACTGGGGAAA	11260 CATAAAAGGA	11270 SAGAAAATACT	11284 TGGGGAAA
11285 11296 11390 11300 11310 11320 11330 11340 11350 11360 JULES 11285 11295	13 (306) 15 (1) 16 (1) 17 (1) 18(11194)		V	5	44441444444444444444444444444444444444	9		45		4
1285 AGTGATAATGCAGAGTTTAAAATATTTTTGTAAAAGTGCCAGAGATTGAGTATAACAAGTGTGACCAAAAAAAA	(11285) 11285	11290	11300	11310	11320	11330	11340	11350		11375
11376	1(11285) AGTGA 1 (2335) AGTGA 3 (306) 5 (1) 6 (1) s(11285)	TAATGCAG! TAATGCAG!	AGTTTAAAAT AGTTTAAAAT AGTTTAAAAT AGTTTAAAAT	ATTTTGTAA ATTTTTGTAA 	AAGTGCCAGA AAGTGCCAGA 	GATTGAGTAT GATTGAGTAT 	AACAAGTGTGAACACAACAACAACAACAACAACAACAACAACAACAACA	ACCAAAAAAA ACCAAAAAAAA 	44444444444444444444444444444444444444	AAAAAAG .AAAAAAG
1376 GAAGAAGGTAAAAAAAAAAAAGAGGTCTGAGAAATAGAAATATCAGAGGAAGGA	(11376) 11376		11390	11400	11410	11420	11430	11440		11466
	1(11376) GAAGA. 1 (2426) GAAGA. 3 (306)	AGGTAAAAA AGGTAAAAA	AAAAGAGGGAO AAAAGAGGGAO	GGTCTGAGAA GGTCTGAGAA	ATAGAAATAT ATAGAAATAT 	CAGAGGAAGG CAGAGGAAGG	AAATAAAGGA AAATAAAGGA 	SGGTGAGAGT, SGGTGAGAGT,	AAATICICIII AAATICICIII 	TAGCATT TAGCATT

SEQ NO 11, 13, 15, 16 and 17 against SEQ NO 1

Consensus(11467) Section 128	11630 AGATCAGAGA AGATCAGAGA 	11620 GTGACAAAA GTGACAAAA GTTTATATATT TTTTATATTT	11700 GAAGGTAAAA GAAGGTAAAA	11690 ATTTGGGTT ATTTGGGTT	11680 GATATAACAT GATATAACAT	11670 ATTGGAGTAG ATTGGAGTAG	11660 AAAAATACAGA AAAAATACAGA	(11558) (11649) 11649 (11649) AACTATCAG (2699) AACTATCAG (2699) AACTATCAG (10)	SEQ ID NO 16 (1) SEQ ID NO 17 (1) Consensus(11558) (11649) 11649 SEQ ID NO 1(11649) AACT SEQ ID NO 11 (2699) AACT SEQ ID NO 13 (306) SEQ ID NO 15 (1) SEQ ID NO 16 (1) Consensus(11649)
1164	11630	11620	ATAGAGAAAA ATAGAGAAAA 	TCTTCAGGA TCTTCAGGA 	TGCTCTAATT TGCTCTAATT 	IGCAGTGGTT IGCAGTGGTT 	AAAAACTATGT AAAAACTATGT	58) GGATGCTAC 18) GGATGCTAC 16)(1)	SEQ ID NO 1(11558) GGAT SEQ ID NO 11 (2608) GGAT SEQ ID NO 13 (306) SEQ ID NO 15 (1)
Section 10 1			11610 ATAGAGAAAA ATAGAGAAAA	11600 TCTTCAGGA TCTTCAGGA	11590 TGCTCTAATT TGCTCTAATT	11580 IGCAGIGGII IGCAGIGGII	SEQ ID NO 1(11558) 11558 EQ ID NO 11 (2608) GGATGCTAGAAAAACTATGTTGCAG' EQ ID NO 13 (306)	(11558) 11558 (11558) GGAIGCIAC (2608) GGAIGCIAC (306)	(11558 NO 1(11558 O 11 (2608 O 13 (306 O 15 (1
SEQ ID NO 11 (2517) CAGATICCACAGATICCACAAATCACATITCITITITACCAACTAAGGAAAATAACACTIGACCTAACATITCATIGCAGTIAGCIAAA			11610 ATAGAGAAAA	11600 TCTTCAGGA	11590 TGCTCTAATT	11580 11580 11580 11580	11570 AAAAACTATGT	(1) (1) (1) (2) 11558 (3) 11558 (4) GGAIGCIAC (8) GGAIGCIAC (1) (1) (1) (1)	SEQ ID NO 13 (306) SEQ ID NO 15 (1) SEQ ID NO 16 (1) SEQ ID NO 17 (1) Consensus(11467) (11558) 11558 SEQ ID NO 1(11558) GGA SEQ ID NO 11 (2608) GGA SEQ ID NO 13 (306) SEQ ID NO 15 (1)

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SEQ NO 11, 13, 15, 16 and 17 against SEQ NO 1

(1174	(11740) 11740	11750	11760	11770	11780	11790	11800	11810	Section 130 11820 1183	າ 130 11830
SEQ ID NO 1(11740) TCAGTTTGGTCCCTGGAACAGCATCAGAATCTGCCGAGGGCTTGTTAAAAAGGCAGAATCTCAGGTCCCATCCCAGACTCACTGAATC SEQ ID NO 11 (2790) TCAGTTTGGTCCCTGGAACAGCATCAGAATCTGCCGAGGGCTTGTTAAAAAGGCAGAATCTCAGGTCCCATCCCAGACTCACTGAATC SEQ ID NO 13 (306)	40) TCAGITT 90) TCAGITT 06) (1)	TGGTCCCTGGF TGGTCCCTGGF 	SEQ ID NO 1(11740) TCAGTTTGGTCCCTGGAACAGCATCAGAATCTGCCGAGGGCTTGTTAAAAAGGCAGAATCTCAGGTCCCATCCCAGACTCACTGAATC FQ ID NO 11 (2790) TCAGTTTGGTCCCTGGAACGCAGCATCAGAATCTGCCGAGGGCTTGTTAAAAAGGCAGAATCTCAGGTCCCATCCCAGACTCACTGAATC FQ ID NO 13 (306)	AGAATCTGCC: AGAATCTGCC: 	GAGGCTTGTT GAGGGCTTGTT 	AAAAAGGCAG FAAAAAGGCAG 	AATCTCAGGT AATCTCAGGT	CCCATCCCAG	ACTCACTGAA ACTCACTGAA 	
SEQ ID NO 17 (1) Consensus(11740)	(1)								Section 131	=
(1183	(11831) 11831	11840	11850	11860	11870	11880	11890	11900	11910 118	11921
SEQ ID NO 1(11831) AGAATATAAAATACTGACAAGATGCCCCGGGATTCATATGCACAGTAGAGCTGGCGAAGTTCCATTGTAGCCTGTGATTGTTTTCTGCAACT SEQ ID NO 11 (2881) AGAATATAAAATACTGACAAGATGCCCCGGGATTCATATGCACAGTAGAGCTGGCGAAGTTCCATTGTAGCCTGTGATTGTTTTCTGCAACT SEQ ID NO 13 (306)	31) AGAATAT 81) AGAATAT 06) (1) (1) (1)	TAAATACTGAC TAAATACTGAC 	2AAGATGCCCCG 2AAGATGCCCCG 	GGATTCATAT GGATTCATAT 	CCGGGATTCATATGCACAGTAGAGCTGGCGAAGTTCCAT CCGGGATTCATATGCACAGTAGAGCTGGCGAAGTTCCAT	3CTGGCGAAG1	TCCATTGTAG TCCATTGTAG	TGTAGCCTGTGATTG TGTAGCCTGTGATTG	TGTTTTCTGCAACT TGTTTTCTGCAACT	H H I I I I I I I I I I I I I I I I I I
(1192	(11922) 11922	11930	11940	11950	11960	11970	11980	11990	12000 120	12012
SEQ ID NO 1(11922) TAGTATTTCTGAGTTTTCCCAAGGA. SEQ ID NO 11 (2972) TAGTATTTCTGAGTTTTCCCAAGGA.	22) TAGTAT 72) TAGTAT	TICIGAGITII TICIGAGIITI	CCCAAGGAAGA	AAACCCAGGC	GCTICI	SGCAGACTIG1 SGCAGACTIG1	GITICICCII	TACTTACTAG TACTTACTAG	CIGCAIGACT	CA
(3)	06)									I I I I
SEQ ID NO 16 SEQ ID NO 17	(1)									
Consensus(11922)	22)									

12103 12103 TGAGGATG 	ATG Section 134	TABACT CTABACT 	TCTAAACT TCTAAACT Section 135	12285 TIAGCAA	TTAGCAA TTAGCAA TTAGCAA
12040 12050 12060 12070 12080 12090 12103 1210		12130	TATTIACAGACCIGCCGCAGACAATICIGCIAGCAGCCITIGIGCIATTATCIGTITICIAAACT TATTIACAGACCIGCCGCAGACAATICIGCIAGCAGCCTITGIGCIATTATCIGTITICIAAACT TATTIACAGACCIGCCGCAGACAATICIGCTAGCAGCCTITGIGCTATTATCIGTITICIAAACT Section 135	12250	TAACTCTGAAATAAATAAGCTGATTTATTTTATTTTCTCAAAACAACAGAATAGGATTTAGCAAAACAAAACAAATTAGCAAAAAAAA
12080 LTCATCTCCT/ LTCATCTCCT/ LTCATCTCCT/		12170 TTTGTGCTA	TTTGTGCTAT	12260 TICAAAACAAC	.10AAACAA(
12070 ACTATAATAA ACTATAATAA 		12160 GCTAGCAGCC GCTAGCAGCC	GCTAGCAGCC	12250 ATITATITE	ATTTATTTC
12060 TAAAATGGAG TAAAATGGAG		AGACAATICT AGACAATICT 	 AGACAATICI AGACAATICI	12240 CIGATIAITE	CTGATTATTTCCTGATTATTTCCTCTCTCTCTTTTTTTTT
12050 TCCTCATCTA TCCTCATCTA		12140 GACCTGCGG GACCTGCCGC	SACCIGCGC GACCIGCGC	12220 12230 12240 TAACTCTGAATAAATAAGCTGATTATT	AATAAATAAG
12040 GCCTGAGT GCCTGAGT		TCTATITACA	I O O	12220 SIBACICIGA	CTAACTCTGAAATAAATAAGCTGATTATT
12030 AAACTITAIG AAACTITAIG		CTITCATICC CTITCATICC	TITCATICC	12210 3A TCTGGAGA	GATCTGGAGA 641011010000000000000000000000000000000
20 AAAIC AAAIC 		7.000.C	JID NO 16 (1)	(12195) 12195 12200 12210 SEQ ID NO 1(12195) TAGTARITGAGTGTGTGATCTGGAGAC	SEQ ID NO 11 (3245) TAGTAATTGAGTGGGGGGGGGGGGGGD NO 13 (306)
SEQ ID NO 1(12013) 12013 120 SEQ ID NO 1(12013) TGAGCAAGG. SEQ ID NO 11 (3063) TGAGCAAGG. SEQ ID NO 13 (306) SEQ ID NO 15 (1)	(12013)	SEQ ID NO 1(12104) 12104 12110 SEQ ID NO 1(12104) 115AACAAAT SEQ ID NO 11 (3154) 115AACAAAT SEQ ID NO 13 (306)	(1210	(12195) 12195 12200 1(12195) TAGTAATTG	SEQ ID NO 11 (3245) TAGTAATTG SEQ ID NO 13 (306) SEQ ID NO 15 (1) SEQ ID NO 16 (1) SEQ ID NO 17 (95) TAGTAATTG
SEQ ID NO 1(SEQ ID NO 11 SEQ ID NO 13 SEQ ID NO 15 SEQ ID NO 15 SEQ ID NO 16	SEQ ID NO 17 (1) Consensus(12013)	SEQ ID NO 1(SEQ ID NO 11 SEQ ID NO 13 SEQ ID NO 13	SEQ ID NO 16 SEQ ID NO 17 Consensus() SEQ ID NO 1(SEQ ID NO 11 SEQ ID NO 13 SEQ ID NO 15 SEQ ID NO 16 SEQ ID NO 16

SEO ID NO 1 (12286) ATTACTCTIAAGATATTATTTTACATTTCTCATCCTCACCTCA	!	(12286) 12286	12300	12310	12320	12330	12340	12350	12360	12376
(1) (1) (1) (1) (1) (1) (1) (1) (1) (1)	VO 1(122 O 11 (33 O 13 (3)	86) ATTACTTC 36) ATTACTTC 06)	TTAAGATATTAT TTAAGATATTAT 	TITACATITC TITACATITC	TATATICICC TATATICICC 	TACCCTGAGT TACCCTGAGT	TGATGTG16/ TGATGTG16/ 	NGCAATATGTU NGCAATATGTU	CACTTTCATAAA CACTTTCATAAA 	SCCAGGTAT SCCAGGTAT
(186) ATTACTTCTIAAGATATTATTTACATTTCTCTACCTCAGGTGAGGGGGGGG	O 15 O 16		1 1					1 1	 	
12370 12390 12410 12420 12430 12440 12450 12460 1254	10 17 (1 ensus(122	86) ATTACTTC 86) ATTACTTC	TTAAGATATTAT TTAAGATATTAT	TITACATITC	TATATICICC TATATICICC	TACCCTGAGT	TGATGTGTG/ TGATGTGTG/	AGCAATATGTA AGCAATATGTA	CACTTTCATAAA	GCCAGGTA GCCAGGTA — Section 13
TATGGACAGGTAAGTAAAAACATATTATTTATTCTACGTTTTTGTCCAAAATTTTAAATTTCAACTGTTGCGGGTGTGTTGGG TATGGACAGGTAAGTAAAAACATATTATTTTTTGTCCAAAAATTTTAAATTTCAACTGTTGCGGGTGTGTTGGG TATGGACAGGTAAGTAAAAACATATTATTTTTTTTTT	(123	77) 12377	12390	12400	12410	12420	12430	12440	12450	12
(277) CATTATEGACAGGTAAAAAACATATTATTTATTCTACGTTTTTGTCCAAAAATTTTAAATTTCAACTGTTGCGCGTGTGTTGGT (2377) CATTATGGACAGGTAAAAAACATATTATTTTATTCTACGTTTTTGTCCAAAAATTTTAAATTTCAACTGTTGCGCGTGTGTTGGT Section (2468) 12468	NO 1(123 10 11 (34 10 13 (3 10 15	77) CATTATES (27) CATTATES (06) (1)	88C8GT88GT88	AAAACATATT AAAACATATT 	ATTIATECTA 	CGTTTTGTC CGTTTTTGTC	CAAAATITI CAAAAATITI 	7AAATTTCAA(CTGTTGCGCGTG	EGTTGGTT
12480	10 17 (2 ansus(123	(7)	BACAGGTAAGTAA	AAAACATATT AAAACATATT.	ATTTATTCTA ATTTATTCTA	CGTTTTTGTC	CAAAAATTT	AAATTCAAC	CTGTTGCGCGTG	TGTTGGTA. TGTTGGTA. — Section 13
AAACAAACTCAGTACAGTATTCAGTACAGTATTTAAGCCCCTGTACTTAAACATATTCCTCGTACCAATGAAGTTACATGAAAAAAAA	(124	68) 12468	12480	12490	12500	12510	12520	12530	12540	125
	NO 1(124 IO 11 (35 IO 13 (31	68) GTAAAACA(18) GTAAAACA(18) GTAAAACA(18)	AAACTCAGTACAG AAACTCAGTACAG	TAGTATICAG TAGTATICAG	TACAGTATIT TACAGTATIT	AAGCCCCTGT AAGCCCCTGT	ACTTAAACA] ACTTAAACA] 	ATICCICGIA ATICCICGIA	ACCAATGAAGTT ACCAATGAAGTT 	ACATGAAA ACATGAAA
	51 01 51 01	1					! ! ! ! !			
	10 10 10 17 (§	 	1 1							

SEQ NO 11, 13, 15, 16 and 17 against SEQ NO 1

Section 139 12649 1GTGTATG 1GTGTATG	12740	CCAAG CCAAG 	Section 141 12831 CATGAAAT CATGAAAT CATGAAAT
Section Sectio	12730	TTAATAAGA TTAATAAGA	12820 AAACAGCAT AAACAGCAT AAACAGCAT AAACAGCAT AAACAGCAT
12630 ITTCAAAAC ITCAAAAAC	12720	SCIGCIAIGA SCIGCIAIGA CIIIII	12810 SAAGAGACA BAAGAGACA SAAAGAGACA
Section 139 12620 12630 12648	12710	CATAAGCTG(CATAAGCTG(CATAAGCTG(CATAAGCTG(CATAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	12800 12810 12820 12831 12830 12831 12830 12831 12830 12831 12830 12831 12830 12831 12830 12831 12830 12831 12830 12831 12830 12831 12830 12831 12830 12831 1283
12610 CCCACAAT CCCACAAAT	12700	000111000110000100000000000000000000000	12790 TITATCAGG TITATCAGG
12600 CITIAIGIIC CITIAIGIIC 	12690	GATACGCTT1 GATACGCTT1 	12780 ATGACTATC1 ATGACTATC1
12590 GGAAGTAAATTAGTCT GGAAGTAAATTAGTCT 	12680	GAGAGACAGAGAGATACGCTTTGGTTGCCTCCATAAGCTGGCTG	SEQ ID NO 1(12741) 12741 12750 12750 12770 12780 12780 12890 12810 12820 12831 SEQ ID NO 1(12741) TITICTAAAGAAAATGAGATCATAACAAAAGCCCTCTTTATGACTATCTTTTATCAGGGGCAAAAGGAAAGAAA
12580 GTAGATGGAA GTAGATGGAA 	12670	GTGTGAGAGA GTGTGAGAGA 	12760 TCATAACAAA TCATAACAAA
SEQ ID NO 1(12559) 12559 12570 12580 SEQ ID NO 1(12559) CAAATTTGTGTGAGATATCGTAGAT SEQ ID NO 11 (3609) CAAATTTGTGTGAGATATCGTAGAT SEQ ID NO 13 (306)	12660	SEQ ID NO 1(12650) TGTGTGTGTGACAGAGTGTGTGTGAASEQ ID NO 11 (3700) TGTGTGTGTGTGACAGAGTGTGTGTGAASEQ ID NO 11 (3700) TGTGTGTGTGTGACAGAGTGTGTGTGAASEQ ID NO 13 (306)	SEQ ID NO 1(12741) 12741 12750 12760 SEQ ID NO 1(12741) TTTTCTAAAGAAAATGAGATCATAA EQ ID NO 11 (3791) TTTTCTAAAGAAAATGAGATCATAA EQ ID NO 13 (306)
59) 12559 59) CAAAIIIGI 509) CAAAIIIGI 506) (1) (1) (1) (25)	12650	650) TGTGTGTGTG 700) TGTGTGTGTG 306) (1) (1) 367)	12741 TTTTCTAAA(TTTTCTAAA(
SEQ ID NO 1(12559) 12559 SEQ ID NO 1(12559) CAAA SEQ ID NO 11 (3609) CAAA SEQ ID NO 13 (306) SEQ ID NO 15 (1) SEQ ID NO 16 (1) Consensus(12559)	(12650) 12650	SEQ ID NO 1 (12650) TGT SEQ ID NO 11 (3700) TGT SEQ ID NO 13 (306) SEQ ID NO 15 (1) SEQ ID NO 16 (1) SEQ ID NO 17 (367) Consensus(12650)	SEQ ID NO 1(12741) 12741 SEQ ID NO 1(12741) TTTT SEQ ID NO 11 (3791) TTTT SEQ ID NO 13 (306) SEQ ID NO 15 (1) SEQ ID NO 16 (1) SEQ ID NO 17 (367) Consensus(12741)
SEQ II SEQ II SEQ II SEQ II SEQ II COI		SEQ II SEQ II SEQ II SEQ II SEQ II	SEQ II SEQ II SEQ II SEQ II SEQ II SEQ II

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Section 142	12922	601010 601010 1	GCICIC	 TGGCTCTC Section 143	13013	ATTCAA ATTCAA ATTCAA	AIICAA	 CCATTCAA Section 144	13104	CAAGCA	 Cargora	 CAAGCA
Sec	12910	SEQ ID NO 1(12832) GATGAGGGCAAGTGATGATTCATTCACATGATTGCTTTCAAGAGTAATTTCTCTTGGGTAATTCAGCAGCCTGTTACTATGGCTCTCT SEQ ID NO 11 (3882) GATGAGGACCAAGTGATGAATTCATTCACAATGATTGCTTTCAAGAGTAATTTCTCTTGGGTAATTCAGCAGCCTGTTACTATGGCTCTC SFO ID NO 13 (306)	TCACAATGATTGCTTTCAAGAGTAATTTCTCTTGGGTAATTCAGCAGCCTGTTACTATGGCTCTC		13000	GCCTCTAAAAGIGGATTATCCTGACAAGAATATACTCAGCCAATAATGCAACAGAAATCCATTCAA GCCTCTAAAAGIGGATTATCCTGACAAGAATATACTCAGCCAATAATGCAACAGAAATCCATTCAA	GCCTCTAAAAGTGGATTATCCTGACAAGAATATACTCAGCCAATAATGCAACAGAAATCCATTCAA	GCCTCTAAAAGTGGATTATCCTGACAAGAATATACTCAGCCAATAATGCAACAGAAATCCATTCAA Section 144	13090	SEQ ID NO 1(13014) AGCATTOGGGAAAATTCAAAAGAATAATTCTTTTTTTTTT	 Tititaaagitaaigacctacgatccattccctcctcactaacca	
	12900	ATTCAGCAGCCAAGCC	ATICAGCAGC	 ATTCAGCAGC	12990	CCAATAATGC) CCAATAATGC!	CARIARIGO	CCAATAATGC/	13080	ATCCATITOT. ATCCATITOT	ATCCATTCT.	
	12890	CTCTTGGGTA. CTCTTGGGTA.	CICIIGGGIA	CICIIGGGIA	12980	ATATACTCAG ATATACTCAG	ATATACTCAG	ATATACTCAG	13070	ATGACCTACG ATGACCTACG	ATGACCTACG	
	12880	AGAGTAATIT AGAGTAATIT	AGAGTAATTI	 AGAGTAATTT	12970	CCTGACAAGA CCTGACAAGA	CCIBACAGA	CCTGACAAGA	13060	TTTAAAGTTA TTTAAAGTTA	 TTTAAAGITA	
	12870	ATTGCTTTCA ATTGCTTTCA	ATTGCTTTCA	ATTGCTTTCA	12960	AGTGGATTAT	AGTGSATIAT	AGTGGATTAT	13050	TTTTTTTTTT	- 8-9 - -1	
	12860	ATTCACAATG ATTCACAATG	i1	ATTCACAATG	12950	AGCCICIAAA AGCCICIAAA	AGCCICIAAA	AGCCICIAAA	13040	ATAAATATIOTT ATAAATATIOTT	ATAAATATICITIT	
	12850	SEQ ID NO 1(12832) GATGAGGGGAGTGATGAAATTCA EQ ID NO 11 (3882) GATGAGACCAAGTGATGAAAATTCA FO ID NO 13 (306)	(35) GAIGAGACCAAGIGAITCA	DID NO 17 (367)	12940	SEQ ID NO 1(12923) IGGACTGATACCTAATGTAATGAA SEQ ID NO 11 (3973) IGGACTGATAGCTAATGTAA SEO ID NO 13 (306)	(126) TGSAGISATAGCTAATGTAAATGAA (1)	OID NO 17 (367)	13030	SEQ ID NO 1(13014) AGCATTCGGGAAAAATTCAAAAGAA EQ ID NO 11 (4064) AGCATTCGGGAAAAATTCAAAAGAA FO ID NO 13	(200)	3 ID NO 17 (367)
	12840	AGACCAAGTG AGACCAAGTG	AGACCAAGIG		12930	STGATAGGTA STGATAGGTA	SIGATAGCIA	STGATAGCTA	13020	TTCGGGAAAA TTCGGGAAAA	 :TCGGGAAAA	
	(12832) 12832	(12832) GATG! (3882) GATG! (306)	(35) GAIGE	(367) (12832) GATGA	(12923) 12923	(12923) TGGAG (3973) TGGAG (306)	_	(367) (12923) IGGAG	(13014) 13014 13020	(13014) AGCA (4064) AGCAS		(1) (367) (13014) AGCAT
		SEQ ID NO 1(12832) GA SEQ ID NO 11 (3882) GA SEQ ID NO 13 (306) ==	SEQ ID NO 15	SEQ ID NO 17 Consensus(SEQ ID NO 1(1 SEQ ID NO 11 (SEQ ID NO 15	SEQ ID NO 17 Consensus(1		SEQ ID NO 1(SEQ ID NO 11	SEQ ID NO 15	SEQ ID NO 17 Consensus(

											Section 145
	(13105) 13105 13110	105 10	3110	13120	13130	13140	13150	13160	13170	13180	13195
SEQ ID NO 1	(13105) GK (4155) GK	78860 78860	ACTTABAB ACTTBABA	SEQ ID NO 1(13105) GCAAGCACTTAAAAATATCCAGCCA EQ ID NO 11 (4155) GCAAGCACTTAAAAATATCCAGCCA	CAGGATGAAA CAGGATGAAA	GGATGAAATAGAAACCCACCTGACTIGI GGATGAAATAGAAACCCACCTGACITGI	SCTGACTIGI SCTGACTIGI	IAATATITI IAATATITI	GTTTGGTCC	SEQ ID NO 1(13105) GCAAGCACTTAAAAATATCCAGCCAGGATGAAATAGAAACCCACCTGACTTGTTAATATTTTTGTTTG	ATTCTAAG ATTCTAAG
SEQ ID NO 13 SEQ ID NO 15	(308) (308) GCAA (4)		 acttaaaa	ATATCCAGE	CAGGATGAAA	(306)(308) GOAAGGACTTAAAAATATAAAAAAGCCCACCTGACTTGT	CICACIIGE	THALLITE		IAATAITITIGITISGICCCAGGGACICAGAI	ATICIAAG
SEQ ID NO 17 Consensus	(367) (13105) GCA	CAAGCA	GCACTTAAAA	 AATATCCAGC		TAGAAACCCA(CCTGACTTGT	 TAATATTTT	GTTTGGTCC	OID NO 17 (367)	
	(13196) 13196	196		13210	13220	13230	13240	13250	13260	13270	13286
SEQ ID NO 1(13196) CCAAA SEQ ID NO 11 (4246) CCAAA	(13196) SK (4246) SK (200)	2 4 4 4 7 7 7 4 4 4 7 7 7 7 7 7 7 7 7 7	TCTTTGAA	SEQ ID NO 1(13196) CCAAATICTTTGAATGATCTTGGCA SEQ ID NO 11 (4246) CCAAATICTTTGAATGATCTTGGCA	CAAAIGICIC CAAAIGICIC	AATGTCTCGAATTATTTTTGCCAACTT AATGTCTCGAATTATTTTTGCCAACTT	FGCCAACTTT FGCCAACTTT	CTTTATCIT TCTTTATCIT	GGAAAAAAA Ggaaaaaaa	AATGTCTCGAATTATTTTTGCCAACTTTTCTTTATCTTGGAAAAAAAGTTTCATGAATGGGTGTCA AATGTCTCGAATTATTTTTGCCAACTTTTCTTTATCTTGGAAAAAAGTTTCATGAATGGGTGTCA	\$0000000000000000000000000000000000000
SEQ ID NO 15	(398) (399) こふ (1) (1)	1주 당 당	TCTTTGAA	TGATCTIGG		GARTERITE				300 399 CCARAITCTITGARICATCTIGGCAAATGICTCGAATIATTITTGCCAACITITCTITATCTTGGAAAAAAAGTTTCATGAAIGGTGTCA 11	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
SEQ ID NO 17 Consensus((367) (13196) CCAAAT		TCTTTGAA	OID NO 17 (367)	CAAATGICIC	GAATTATTT	 IGCCAACIII	 ICTTTATCTT	 GGAAAAAAA		GGGTGTCA
	(13287) 13287	287	5	13300	13310	13320	13330	13340	13350	13360	13377
SEQ ID NO 1 SEQ ID NO 11	(13287) <i>83</i> (4337) 83	ANTIC ANTIC	ATTAGTTT ATTAGTTT	SEQ ID NO 1(13287) AAATTGATTAGTTTTAAAAACCTTT EQ ID NO 11 (4337) AAATTGATTAGTTTTAAAAACCTTT	TICTIGCAGA	TACGIATGGC TACGIATGGC	ACCCIARAC	TGTATTAGAA TGTATTAGAA	AAAAAGTAA AAAAAGTAA	SEQ ID NO 1(13287) AAATTGATTAGTTTTAAAAACCTTTCTTGCAGATACGTATGGCACCCTAAAACTGTATTAGAAAAAAGTAAGT	TGTGAAAA
SEQ ID NO 13 SEQ ID NO 15		- I I I I I I	ATTAGTTE	 Taaaaact	TTCTTGCAGA	(306)	a	 IGTATTAGAA	 ####		
SEQ ID NO 16 SEQ ID NO 17	9	 									
Consensus	(13287) A J	AATIG	ATTAGTTT	TAAAAACCT	TICITGCAGA	Consensus(13287) AAATIGATIAGITITIAAAAACCTITICIIGCAGAIACGIAIGGCACCCIAAAAACIGIAIIAGAAAAAAA	ACCCTAAAAC	IGTATTAGAA	AAAAA		

SEQ NO 11, 13, 15, 16 and 17 against SEQ NO 1

13468	CTATATACC CTATATATA	13559	36066666666666666666666666666666666666	13640 13650 GGGTGTGGTGA GGGTGTGGTGA
13450	GTTATTGCTTTC GTTATTGCTTTC GTTATTGCTTTC 	13540	TGGGAGGCCAA(13630 136. AAAATCACCGGG
13440	CTCACAAAAACAGCCTTTGGAATACCCACATGAAGTAGCTGTTGTTATTGCTTTCTATATACC CTCACAAAAACAGCCTTTGGAATACCCACATGAAGTAGCTGTTGTTATTGCTTTCTATATACC	13530	TITIGGCAGGIGIGGCICACACCIGIAATICCAGCACTITIGGGAGGCCAAGGCGGGCGG	13620 15 TGAAAATACAA TGAAATACAA
13430	ATACCCACATG ATACCCACATG	13520	CACACCTGTAA CACACCTGTAA 	13610 CCAGTCTTTAC CCAGTCTTTAC
13420	CAGCCTTTGGA	13510	H	13600 TATGGTGAAAC TATGGTGAAAC
13410	CTCACAAAAACCTCACAAAACCTCACAAAAC	13500	TTTTGGCAGG	13590 GCCTGATCAA1
13400	CTTTTACAAA	13490	AAAAGACTGG	13580 ITTCAGGACCA ITTCAGGACCA
13390	AAGGACACCT AAGGACACCCT 	13480	IGICTATTATA IGICTATTATA 	13570 SAGATCAGGAG SAGATCAGGAG
(13378) 13378	3378) ATTCTTA 4428) ATTCTTA (306) (558) (1) (367)	(13469) 13469	SEQ ID NO 1(13469) TACATCTTGTCTATTATAAAAAGACTGG SEQ ID NO 11 (4519) TACATCTTGTCTATTATAAAAAGACTGG SEQ ID NO 13 (306)	SEQ ID NO 1(13560) ATCACCTGAGATCAGGACCAGCCTGATCAATATGGTGAAACCCAGTCTTTACTGAAAATACAAAAATCACCGGGTGTGGTGA SEQ ID NO 1(13560) ATCACCTGAGATCAGGACCAGCCTGATCAATATGGTGAAACCCAGTCTTTACTGAAAATACAAAAATCACCGGGTGTGGTGA SEQ ID NO 11 (4610) ATCACCTGAGATCAGGACTCAGCTGATCAATATGGTGAAAACCCAGTCTTTACTGAAAATCACACGGGTGTGGTGA SEQ ID NO 13 (306)
5)	SEQ ID NO 1(13378) SEQ ID NO 11 (4428) SEQ ID NO 13 (306) SEQ ID NO 15 (558) SEQ ID NO 16 (1) SEQ ID NO 17 (367) Consensus(13378)	E	SEQ ID NO 1(13469) TACAT SEQ ID NO 11 (4519) TACAT SEQ ID NO 13 (306) SEQ ID NO 15 (558) SEQ ID NO 16 (1) SEQ ID NO 17 (367) Consensus(13469)	SEQ ID NO 1(13560) ATCAC SEQ ID NO 1(13560) ATCAC SEQ ID NO 11 (4610) ATCAC SEQ ID NO 13 (306) SEQ ID NO 15 (558) SEQ ID NO 16 (1) SEQ ID NO 17 (367) Consensus(13560)

SEQ NO 11, 13, 15, 16 and 17 against SEQ NO 1

SEQ ID NO 15 (558) SEQ ID NO 16 (1) SEQ ID NO 17 (367) Consensus(13651)	(358) (1) (367) (13651)		SEQ ID NO 15 (558)						Section 152	 n 152
SEQ ID NO 1(13742) 13/442 SEQ ID NO 11 (4792) CACTG SEQ ID NO 13 (306) SEQ ID NO 15 (558) SEQ ID NO 16 (1) SEQ ID NO 17 (367) Consensus(13742)	(13742) 13742 (13742) CACTG (4792) CACTG 3 (306) 5 (558) 7 (367) (13742)	19/30 3CACTCCAGCCJ 3CACTCCAGCCJ	13/42 13/50	NAGACTCCAT	TSTRO CTCAAAAAA CTCAAAAAA CTCAAAAAA	13/30 AAAAAAAAAA AAAAAAAAAA 	136UU AAGACTGGTT AAGACTGGTT	TITCAACAGCI TITCAACAGCI TITCAACAGCI	1382U	13833 CCTC CCTC
1)	(13833) 13833	13840	13850	13860	13870	13880	13890	13900	13910	13923
SEQ ID NO 1(13833) 1GC SEQ ID NO 11 (4883) 1GC SEQ ID NO 13 (306) SEQ ID NO 15 (558) SEQ ID NO 16 (1) SEQ ID NO 17 (367)	3833) TGCA1 (4883) TGCA1 (306) (558) (1)	SEQ ID NO 1(13833) TGCATGGAAATATTCACCCAGTCAAT SEQ ID NO 11 (4883) TGCATGGAAATATTCACCCAGTCAAT SEQ ID NO 13 (306)	\varTheta \varTheta \blacksquare \blacksquare \blacksquare	HTTTCCTAG1	TTGGGTAAT TTGGGTAAT	0 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	GCAGGACTGG GCAGGACTGG GCAGGACTGG	TGITITCCTAGITIGGGIAAIGGCCCTCTGGGCAGGACTGGAGIGGGCACACAGGAGAAGCTGC TGITITCCTAGITIGGGIAAIGGCCCTCTGGGCAGGAGTGGGGCACACACAGGAGAAGCTGC TGITITCCTAGITIGGGIAAIGGCCCTCTGGGCAGGACTGGAGTGGGGCACACACAGGAGAAGCTGC	ACAGGAGAAA ACAGGAGAAGAAGAAGAGAGAGAGAGAGA	0 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Consensus(13833)	3833)									

SEQ NO 11, 13, 15, 16 and 17 against SEQ NO 1

SEQ ID NO 1(13924) 13924 13930 13940 13950 13960 13970 13980 13980 14000 14014 SEQ ID NO 1(13924) AAACTATGTTTAGAAGCATGTCTGGGAAATGTCATGCAAGAAAGGCATGTTTAAAGGTAGGCATTGCATGAAAAGGAAATGTCATGCAAGAAAAGACATTTTAAAGGTAGGCTTTGCATGCA	14080 14090 14105	SEQ ID NO 1(14015) CTATGTAGAGCCTCTTACTTGCAGTGAGAGAAGCTGGGGAAGCAAGAGCAAGAGCAAGAGCAAGAGCAAGAGCAAGAGCTGCCAAATTTGCAGCTGCCAAATTTGCAGGTGCAGTGAGTG	SEQ ID NO 1(14106) AGGAGGATTGGCTCATCTTGGCTGAGGCTCATGAAACCAGGTGTAAAGAAAG
13980 TAAAGGTAG TAAAGGTAG	14070	CAAGAGGAA CAAGAGGAA 	14160 AAAGIGGAC AAAGIGGAC
13970 AAGACATATT AAGACATATT	14060	NGT GG GG AA G	14150 AGGTGTAAAG AGGTGTAAAG
13960 ATGCAAGAAAATGCAAGAAAAAAAAAAAAAAAAAAAAAA	14050	AGAAGCAAA/ AGAAGCAAA/ 	14140 CATGAAACCACATGAAACCACACACACACACACACACACA
13950 5GGAAATGTC 6GCAAATGTC 	14040	TTGCAGTGAGTTGCAGTGAGTTGCAGTGAGTGAGTGAGTG	14130 3GCTGAGGCT 3GCTGAGGCT
13940 AAGCATGTCT(AAGCATGTCT(14030	AGCCTCTTACC AGCCTCTTACC	14120 CAGTCATCTT CAGTCATCTT
SEQ ID NO 1(13924) 13924 13930 SEQ ID NO 1(13924) AAACTATGTTTAGA SEQ ID NO 11 (4974) AAACTATGTTTAGA SEQ ID NO 13 (306)	(14015) 14015 14020	SEQ ID NO 1(14015) CTATGTAGAGCAGAGCCTCTTACTT EQ ID NO 11 (5065) CTATGTAGAGCAGAGCCTCTTACTT EQ ID NO 13 (306)	(14106) 14106 1(14106) AGGAGGATTGGCTC 1 (5156) AGGAGGATTGGCTC 3 (306)
SEQ ID NO 1(13924) 13924 SEQ ID NO 1(13924) AAACT SEQ ID NO 11 (4974) AAACT SEQ ID NO 13 (306) SEQ ID NO 15 (558) SEQ ID NO 16 (1) SEQ ID NO 17 (367)	į.	SEQ ID NO 1(14015) CTAT SEQ ID NO 11 (5065) CTAT SEQ ID NO 13 (306) SEQ ID NO 15 (558) SEQ ID NO 16 (1) SEQ ID NO 17 (367) Consensus(14015)	SEQ ID NO 1(14106) AGG. SEQ ID NO 1(14106) AGG. SEQ ID NO 11 (5156) AGG. SEQ ID NO 13 (306) SEQ ID NO 15 (558) SEQ ID NO 16 (1) SEQ ID NO 17 (367)

SEQ NO 11, 13, 15, 16 and 17 against SEQ NO 1

								Section 157
(14197) 14197	14210	14220	14230	14240	14250	14260	14270	14287
SEQ ID NO 1(14197) AGCCGTGAAAGATAATCCAGAAATCATTGGGATTTGATGGTAGAAGGTATT	AAGATAATCCAG	SAAATCATIGO	SGATTTGATG	STAGAAGGTAI	TTTGGGACT	ATTCCATTTG?	ITGGGACTATTCCATTTGAAATGAGAAGGTACCTGACATT	CIGACAII
SEQ ID NO 11 (5247) AGCCGTGAAAGATAATCCAGAAATCATTGGGATTTGATGGTAGAAGGTATTTTGGGACTATTCCATTTGAAATGAGAAGGTACCTGACATT SEQ ID NO 13 (306)	AAGATAATCCAG 	3AAATCATTG(3GATTTGATG(3TAGAAGGTAT 	FTTTGGGACTA	ATTCCATTIGA 	AAATGAGAAGGTAC 	CIGACAII
SEQ ID NO 16 (1) SEQ ID NO 17 (367)								
Consensus(1419/)								Section 158
(14288) 14288	14300	14310	14320	14330	14340	14350	14360	14378
SEQ ID NO 1(14288) CITIGAAIICCITICAAGCAAAGGA	ICCTTTCAAGC?	AAAGGATTAAA	ATTACCCATO	SAGTIGACICA	4GAAAAAACA	FAAAAGTAT	TTAAATTTACCCATGAGTTGACTCAGAAAAACATAAAAGTATTGTTGCTCTGCTCAGAGTTTTA	GAGITITA
SEQ ID NO 13 (338) CITIGAATICCITICAAGGAAAGGA	ICCITICAAGC?	\vdash	ATTACCCAT(SAGTTGACTCA	AGAAAAAACA:	LAAAAAGTAT:	TAAATTTACCCATGAGTTGACTCAGAAAAACATAAAAAGTATTGTTGCTCTGCTCAGAGTTTTA	GAGITITA
SEQ ID NO 15 (558)								
SEQ ID NO 16 (1)								
SEG ID NO 17 (307) Consensus(14288)	 	 	; 	 	 	 	 	
								Section 159
(14379) 14379	14390	14400	14410	14420	14430	14440	14450	14469
SEO ID NO 1(14379) TCTAACTCCACTTCTCACTTCTTATTCCATGACATGACA	A T T C T C A C T T C J	TATICCATGA	ATGAAATGACA	CATGATGAATGACATAAATGAGGT	TITITAT	IGITGITGI	TGTTTTCTGGACACAAGGCAAG	AAGGCAAG
SEQ ID NO 13 (306)					1 4 1 1 1 1 1) () () () () () () () () () (044)0044
<u>u)</u>								
SEQ ID NO 16 (1)								
SEQ ID NO 17 (367) Consensus(14379)	! ! ! ! !	 	 	! ! ! ! !	· 	· 		

SEQ NO 11, 13, 15, 16 and 17 against SEQ NO 1

Section 160 0 14550	TGTTCCCA TGTTCCA TGTTCA TGTTCA TGTTCCA TGTTCCA TGTTCA TGTTCA TGTTCA TGTTCA	14651	CATCAGCC CATCAGCC	14742	CCTAAA
Seci 14550	ATTAAGATGT ATTAAGATGT	14640	TCTCTCCCAT TCTCTCTC	14730	GCCCCTTATC
14540	AAGGCAGTC	14630	3ATGACAATG 3ATGACAATG	14720	GCCTGATTG
14530	ATTTCTCTATGCCGTGGAGAGAAATTGGTTAATTGGCCATGGAAGGCAGTCATTAAGATGTTCCCAAAATTCTCTCTATGCCGTGGAAGGCAGTCATTAAGATGTTCCCAAAATTCTCTCTATTAAGATGTTCCCAAAATTCTCTCTATTAAGATGTTCCCAAAATTCTCTCTATTAAGATGTTCCCAAAATTCTCTCTATTAAGATGTTCCCAAAAAAAA	14620	ATTGTTGGTG ATTGTTGGTG ATTGTTGGTG ATTGTTGGTG ATTGTTGGTG ATTGTTGGTG	14710	AAATTIGCTITCAGGAAAAATTITGAAAATGIGTCCAGIAATGCCTGATTGGCCCCTTATCCTAAAAAATTITGGTCCTTATCCTAAAAAATTITGAAAAATGTGTCCAGTAATGCCTGATTGGCCCCTTATCCTAAAAAATTITGGTCCAGTAATGCCTGATTGGCCCCTTATCCTAAAAAATTTTGCTAAAAAATGTGTCCAGTAATGCCTGATTGGCCCCTTATCCTAAAAAATTTTGGTCCTAAAAAAAA
14520	AATTGGTTAAAATTGGTTAAAATTGGTTAAAATTGGTTAAAATTAAAAATTAAAAATTAAAAATTAAAAATTAAAA	14610	CCTCAATTCC CCTCAATTCC	14700	TTGAAAATGT TTGAAAATGT
14510	2GTGGAGAGA 2GTGGAGAGA 1	14600	CTTCCCTGTC CTTCCCTGTC CTTTCCCTGTC	14690	AGGAAAAATT AGGAAAAAATT
14500	TCTCTATGC(14590	TTCTGCATCCTTCTGCATCCCTTCTTCTTCTTCTTCTTCTTCTTCTTTCT	14680	TTTGCTTTCZ
14490	CTGTTTTATT CTGTTTTATT	14580	GGTTCCCAGC GGTTCCCAGC	14670	TTTATTAAAA TTTATTAAAA
14480	CTGGGCAGAGCTGGGCAGAGCTGGCAGAGCAGAGCAGAG	14570	AACTITCCAG	14660	TTCTCTCTCA
(14470) 14470	70) GTAGCTAC 20) GTAGCTAC 36) 38) 37)	(14561) 14561	561) TGCGAGTGA 311) TGCGAGTGA 306) 558) (1) 367)	(14652) 14652	52) TCATGAAG D2) TCATGAAG D6) 58) (1) 57)
(1447)	SEQ ID NO 1(14470) GTAGCTACCTGGGCAGAGCTGTTTT/SEQ ID NO 11 (5520) GTAGCTACCTGGGCAGAGCTGTTTT/SEQ ID NO 13 (306)	(1456	SEQ ID NO 1(14561) TGCGAGTGAACTTTCCAGGGTTCCCAGCTTCTGCATCCTTCCT	(146	SEQ ID NO 1(14652) TCATGAAGTTCTCTCTCTTTATAAATTTGCTTTCAGGAAAAATTTTGAAAATGTGTCCAGTAATGCCTGATTGGCCCCTTATCCTAAA SEQ ID NO 11 (5702) TCATGAAGTTCTCTCTCTCTTTATTAAAATTTGCTTTCAGGAAAAATTTTGAAAATTTTGAAAATTTGAAAATTTGAAAAATTTGAAAAATTTGAAAAATTTGAAAAATTTGAAAAATTTGAAAAATTTGAAAAATTTGAAAAATTTGAAAAATTTGAAAAAA

SEQ NO 11, 13, 15, 16 and 17 against SEQ NO 1

SEQ ID NO 15 (588) SEQ ID NO 17 (367) Consensus(14743) SEQ ID NO 1(14834)	SEQ ID NO 11 (5793) GGCTTA SEQ ID NO 13 (306) SEQ ID NO 15 (558) SEQ ID NO 16 (1) SEQ ID NO 17 (367) Consensus(14743) SEQ ID NO 1(14834) 14834	(14743) GGCTTAP (5793) GGCTTAP (306) (558) (10) (367) (14743) (14834) 14834 1	14750 AACTGGAG AACTGGAG	SEQ ID NO 1(14743) 14750 14760 SEQ ID NO 1(14743) GGCTTAAACTGGAGGAAGGAAGCTAAGEO ID NO 11 (5793) GGCTTAAACTGGAGGAAGGAAGCTAAGEO ID NO 11 (5793) GGCTTAAACTGGAGGAAGGAAGCTAAGEO ID NO 13 (306)	SEQ ID NO 1(14743) 14750	14770 14780 14800 14810 14820 14830 AACTGAGAAATCTTGAGCCAAAAACGTATTAATAGCAAGATCTATCATTTATTGAC	14790 CATTGAGCCACATTGAGCCACATTGAGCCACATTGAGCCACATTGAGCCACATTGAGGGGGGGG	14800 AAAACGTATT AAAACGTATT	14810 AATAGCAAGA AATAGCAAGA AATAGCAAGA AATAGCAAGA AATAGCAAGA AATAGCAAGA AATAGCAAGA AATAGCAAGA AATAGCAAGAAAAAAAAAA	14820 TCTATCATT: TCTATCATT: TCTATCATT: TCTATCATT: TCTATCATT: TCTATCATT: S6	14833 TTATTGAC TTATTGAC Section 164 14924
SEQ ID NO 11 (5884) TAG SEQ ID NO 13 (366) SEQ ID NO 15 (558) SEQ ID NO 16 (1) SEQ ID NO 17 (367) Consensus(14834)	(5884) TAGT (306) (558) (1) (367) (4834)	G T T T C C C C C C C C C C C C C C C C	0 0 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	H H	SEQ ID NO 11 (5884) TAGTATGTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	AGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	0 0 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	7	ACATCITARA	S	ATCTCCTC ATCTCCTC ATCTCCTC ATCTCTCTC ATCTCTCTC
(14925) 14925 SEQ ID NO 1(14925) CTAT. SEQ ID NO 11 (5975) CTAT. SEQ ID NO 13 (306) SEQ ID NO 15 (558) SEQ ID NO 16 (1) SEQ ID NO 17 (367)	(14925) 14925 14930 (14925) CTATATAAA (5975) CTATATAAA (306) (558)	225 14 ATAT/ ATAT/ 	930 AAATCATG AAATCATG 	14940 TAAGICAAGA TAAGICAAGA 	SEQ ID NO 1(14925) 14925 14930 15000 15015 SEQ ID NO 1(14925) CTATATAAATCATGTAAAGGAATTGTCTTTGTTTTGTTT	14960 TTGTCTTTGTT TTGTCTTTGTT	14970 TGGTTATATT TGGTTATATT	14980 CAGGGGATTI CAGGGGATTI	14990 AGAGTATACAGAGAGTATACAG	15000 TAGAAGATCC TAGAAGATCC	15015 CCAAGAA CCAAGAA

SEQ NO 11, 13, 15, 16 and 17 against SEQ NO 1

SEQ ID NO 1(5016) 15016 15030 15040 15050 15060 15070 15080 15106 SEQ ID NO 1(15016) ACCTTGGGATCATTTTAGACTAAGAAATGCCAATACCGCCGGGCGGG	15130 15140 15150 15160 15170 15180 15197	TGAGACCGICCTGGCTAACGTGGTGAAACCCTGTCTCTACTAAAAATACAAAAATTAGCCGGGCGTGG TGAGACCGTCCTGGCTAACGTGGTGAAACCCTGTCTCTACTAAAAATACAAAAATTAGCCGGGCGTGG	15230 15240 15250 15260 1527
15030 15040 TITAGACTAAGAAAT	15120 15130	TCAGGAGATTGAGACC	15210 15220 GTAGTCCCAGCTACTC GTAGTCCCAGCTACTC
SEQ ID NO 1(15016) 15016 SEQ ID NO 1(15016) ACCTTGGGATCATTTTAGACTAAGA SEQ ID NO 11 (6066) ACCTTGGGATCATTTTAGACTAAGA SEQ ID NO 13 (306)	(15107) 15107	SEQ ID NO 1(15107) GCGGATCACAAGGTCAGGAGATTGA SEQ ID NO 11 (6157) GCGGATCACAAGGTCAGGAGATTGA SEQ ID NO 13 (306)	15220 15220 15220 15220 15220 15220 SEQ ID NO 1(15198) TGGCGGGCGCCTGTAGTCCCAGCTA SEQ ID NO 11 (6248) TGGCGGGCGCCTGTAGTCCCAGCTA SEQ ID NO 13 (306)

SEQ NO 11, 13, 15, 16 and 17 against SEQ NO 1

								Section 169	69
(15289) 15289	15300	15310	15320	15330	15340	15350	15360	7	15379
SEQ ID NO 1(15289) CCCCAATGCACTCCAGCCTGGGCGA	AATGCACTCCAG	CCTGGGCGACAC	AACGAGACTC	CGICICAGA	CAAAACAAA	CAGAACGAGACTCCGTCTCAGAACAAACAAAGGAAATGCCAATACCAGCAGAAATAGAGCCAAA	ATACCAGCAG	AAATAGAGCCA	AAA
SEQ ID NO 11 (6339) CCCCAATGCACTCCAGCCTGGGCGA SEQ ID NO 13 (306)	AATGCACTCCAG	CCTGGGCGACAC	AACGAGACTC	CGTCTCAGAA	CAAAACAAAA	CAGAACGAGACTCCGTCTCAGAACAAACCAAAAGGAAATGCCAATACCAGCAGAAATAGAGCCAAA	ATACCAGCAG	AAATAGAGCCA	A
OUISEIISUS(13203)								Section 170	20
(15380) 15380	15390	15400	15410	15420	15430	15440	15450	15460 1	15470
SEQ ID NO 1(15380) TCATGAACATAAGCTAAACAAATGT	SAACATAAGCTA	AACAAATGITGO	CAGIGIAGCC	TAGTGGTTA	AGAGAGCAGAC	TGGCAGTGTAGCCTAGTGGTTAAGAGAGCAGACTCTTAACTAGAACACTGCACTCCATGTCCTCAC	AACACTGCAC	ICCAIGICCI	CAC
SEQ ID NO 11 (9430) TCATGAACATAAGCTAAACAAATGT SEQ ID NO 13 (306)	3AACATAAGCTA/	AACAAIGIIG 	CAGTGTAGCC	TAGTGGTTAA	16	TGGCAGIGIAGCCIAGIGGIIAAGAGAGCAGACICIIAACIAGAACACIGCACICCAIGICCICACICA	AACACTGCAC	FCCATGTCCTC) C
SEQ ID NO 17 (367) Consensus(15380)						 			71
(15471) 15471	15480	15490	15500	15510	15520	15530	15540	15550 18	15561
SEQ ID NO 1(15471) TGTAGACCCTCACTGTGGGGTTCTA. SEQ ID NO 11 (6521) TGTAGACCCTCACTGTGGGGTTCTA.	SACCCICACIGI(SACCCICACIGI(GGGGTTCTAAT]	AACCCCIGII AACCCCIGII	ACTIACCAG:	GGCAGICIIP	ATTAACCCCTGTTACTTACCAGTGGCAGTCTTAAGGCATTCCTTAAGTTCGTTGTGCCCCAATTTG ATTAACCCCTGTTACTTACCAGTGGCAGTCTTAAGGCATTCCTTAAGTTCGTTGTGCCCCCAATTTG	TAAGIICGII(TAAGIICGII(STGCCCCAAT	rrg rrg
ت ت									
SEQ ID NO 16 (1)									
Consensus(15471)									

SEQ NO 11, 13, 15, 16 and 17 against SEQ NO 1

15600 15640 15652 15630 15640 15652 TACTITATAGGCITACTGIGAGCATTAAATGAGTTACTACTGTATTTGTAAAGTGC TACTITATAGGCTTACTGIGAGCATTAAATGAGTTACTACTGTATTTGTAAAGTGC TACTITATAGGCTTACTGTGAGCATTAAATGAGTTACTACTGTATTTGTAAAGTGC TACTITATAGGCTTACTGTGAGCATTAAATGAGTTACTACTGTAAAGTGC TACTITATAGGCTTACTGTGAGCATTAAATGAGTTACTACTGTATTTGTAAAGTGC TACTITATAGGCTTACTGTGAGCATTAAATGAGTTACTACTGTATTTGTAAAGTGC TACTITATAGGCTTACTGTGAGCATTAAATGAGTTACTACTGTATTTGTAAAGTGC TACTITATAGGCTTACTGTGAGCATTAAATGAGTTACTACTGTATTTGTAAAGTGC TACTITATAGGCTTACTGTGAGCATTAAATGAGTTACTACTGTAATTTGTAAAGTGC TACTITATAGGCTTACTGTGAGCATTAAATGAGTTACTACTGTATTTGTAAAGTGC TACTITATAGGCTTACTGTGAGCATTAAATGAGTTACTACTGTATTTGTAAAGTTGC TACTITATAGGCTTACTGTGAGCATTAAATGAGTTACTACTGTATTTGTAAAGTTGC TACTITATAGGCTTACTGTGAGCATTAAATGAGTTGCAGTAGTAGTGCAGTAGTAGTGCAGTAGTAGTGCAGTAGTAGTGCAGTAGTAGTGCAGTAGTAGTAGTGCAGTAGTAGTGCAGTAGTAGTGCAGTAGTAGTGCAGTAGTAGTGCAGTAGTAGTGCAGTAGTAGTGCAGTAGTAGTGCAGTAGTAGTGCAGTAGTAGTGCAGTAGTAGTGCAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTA	15730 15743	GITAAACACTTAAGAACTGATTTACTTGCATCTAAACTGACAGCTCTCAATAACTGGAAATGATCA GITAAACACTTAAGAACTGATTTACTTGCATCTAAACTGACAGCTCTCAATAACTGGAAATGATCA CONTRACACTTAAGAACTGATTTACTTGCATCTAAACTGACAGCTCTCAATAACTGGAAATGATCA CONTRACACTTAAGAACTGAATTACTTGCATCTAAACTGACAGCTCTCAATAACTGGAAATGATCA CONTRACACTTAAGAACTGAAATGATCAAACTGAAACAATAACTGAAATGATCA CONTRACACTTAAGAATGAATGAATGAATGATCAAACTGAAATGATCAAACTGAAATGATCAAAACTGAAATGATCAAAAAAAA	15820 15834	SEQ ID NO 1(15744) AGCATAGGCCCTGGAATATAAGCAGGTCTACATGAAGGCAAAAATGTTCGTTTCTTTTGTTCAGCCCTGTGCCTAGATCAATATCTAGTGA EQ ID NO 11 (6794) AGCATAGGCCCTGGAATATAAGCAGGTCTACATGAAGGCAAAAATGTTCGTTTCTTTTGTTCAGCCCTGTGCCTAGATCAATATCTAGTGA EQ ID NO 13 (306)
15630 GAGITACTAC GAGITACTAC	15720	CAGCTCTCAA'	15810	CCTGTGCCTA(
15620 GAGCATTAAAT GAGCATTAAAT	15710	ATCTAAACTGA ATCTAAACTGA	15800	TTTTGTTCAGG
15610 AGGCTTACTGT AGGCTTACTGT	15700	SATTACTIGC SATTTACTIGC	15790	ATGTTCGTTTC ATGTTCGTTTC
15600 TITACITIAL; TITACITIAL; 	15690	CITAAGAACI CITAAGAACI 	15780	GAAGGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
15590 GACAGTAGTGTT GACAGTAGTGTT	15680	TTGTTAAACA TTGTTAAACA	15770	AGGICTACAT AGGICTACAT
15580 1GGGGTAGGAT 1GGGGTAGGAT	15670	CCAAAGGGGCCCCAAAGAGGGCCCCAAAGGGGGGGGGG	15760	GGATATAAGC GGATATAAGC
2 15570 ATCTGTAGAAATCTGTAGAAATCTGTAGAAAAAAAAAAA	3 15660	AAATGCTGCT AAATGCTGCT 	4 15750	ATAGGCCCTG
SEQ ID NO 1(15562) 15562 15570 15580 SEQ ID NO 1(15562) TTCATCTGTAGAAGGGGTAGGATGA SEQ ID NO 11 (6612) TTCATCTGTAGAAGGGGTAGGATGA SEQ ID NO 13 (306)	(15653) 15653	SEQ ID NO 1(15653) TTAAAATGCTGCTCCAAAAGAGTTT SEQ ID NO 11 (6703) TTAAAATGCTGCTCCAAAAGAGTTT SEQ ID NO 13 (306)	(15744) 15744 15750	SEQ ID NO 1(15744) AGCATAGGCCCTGGAATATAAGCAGGSEQ ID NO 11 (6794) AGCATAGGCCCTGGAATATAAGCAGGSEQ ID NO 13 (306)

SEQ NO 11, 13, 15, 16 and 17 against SEQ NO 1

SEQ ID NO 11 (6885) TCA SEQ ID NO 13 (306) SEQ ID NO 15 (558)	(15835) 15840 15850 SEO ID NO 1(15835) 15870 SEO ID NO 1(15835) 158750 15875	15850 * * * * * * * * * * * * * * * * * * *	15860 FKK7FKK7F	15870	15880	15890	15900	CARCI UNECI	15925
SEQ ID NO 16 (1) SEQ ID NO 17 (367) Consensus(15835)	SEQ ID NO 11 (6885) ICATGCTCAAGAATATTGTTGAAT SEQ ID NO 13 (306)	ATATIGITGAAAATATTGTTGAAAAAAAAAAAAAAAAAA	TGAAICAAI TGAATCAAI	GAACCIACC GAACCIACCI GAACCIACCI 	AGGIAGIIA AGGIAGIIA 	CATAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	TCTGCA1GAG	GAATCAAIGAACCIACCGAGGTAGIIACAIAAAAGAGIICIGCAIGAGIACAAAICIGGGCAAAAGIGAATCAAIGAACIACGAAAGIIGAGIACGAAAGIIGAGIACGAAAGIIGAGIACGAAAGIIGAGIACGAAAGIIGAGIACGAAATCTGGGGCAAAGIIGAGIACGAATCTGGGGCAAAGIICTGAATCTGGGGCAAAGIICTGAATCTGGGGCAAAGIICTGGGGCAAAGIICTGGGGCAAAGIICTGGGGCAAAGIICTGGGGCAAAGIICTGGGGCAAAGIICTGGGGCAAAGIICTGGGGCAAAGIICTGGGGCAAAGIICTGGGGCAAAGIICTGGGGCAAAGIICTGGGGCAAAGIICTGGGGCAAAGIICTGGGGCAAAGIICTGGGGCAAAGIICTGGGGGAAGIICTGGGGGGAAGIICTGGGGGGGGGG	GGCAAAGT GGCAAAGT
(15926) 15926	15926	15940	15950	15960	15970	15980	15990	16000	16016
SEQ ID NO 1(15926) GAC SEQ ID NO 11 (6976) GAC SEQ ID NO 13 (306) SEQ ID NO 15 (558) SEQ ID NO 16 (1) SEQ ID NO 17 (367) Consensus(15926)	SEQ ID NO 1(15926) GACCTCCAAGGAAATTTCCACTTTT SEQ ID NO 11 (6976) GACCTCCAAGGAAATTTCCACTTTT SEQ ID NO 13 (306)	ATTTCCACTTT ATTTCCACTTT	AGATICI AGATICI 	TGATTICCTT	AAGGAACTG AAGGAACTG 	ATAAATTGGTC ATAAATTGGTC 	3TGATACAATG STGATACAATG 	AGATTCTGTGATTTCCTTAAGGAACTGATAAATTGGTGTGATACAATGTAAAAAAATGTGCCTATA AGATTCTGTGATTTCCTTAAGGAACTGATAAATTGGTGTGTGATACAATGTAAAAAAATGTGCCTATA	TGCCTATA TGCCTATA
(16017)	16017	16030	6040	16050	16060	16070	16080	16090	16107
SEQ ID NO 1(16017) TGA SEQ ID NO 11 (7067) TGA SEQ ID NO 13 (306) SEQ ID NO 15 (558) SEQ ID NO 16 (1) SEQ ID NO 17 (367)	TTTGAGAAA.	ACTTATTTTCT 	CTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	HILL CCHICC	TTCCTTTCCTTTCCTTTTTTTTTTTTTTTTTTTTTTTT	000		CCCTCTTTTTTTCCTTCCTTCCTCCCTCCCTTCCTTCC	0001111

SEQ NO 11, 13, 15, 16 and 17 against SEQ NO 1

Section 178 16198 CTCTTCTC CTCTTCTC		16289		Section 180 0 15380	TAAAC TAAAC
Section 178 16198 LITCITCITCITCIC			TCTTTCTGCCTTTC TCTTTCTGCCTTTC	Section 16370	TAAAAGGT
16180 TITCITIC		16270	CCTTTCTT:	16360	TTTTCTAG
16170 CITICITIC		16260	TTCTTTCTT TTCTTTCTT	16350	TGAATGCCT
16160 16170 16180 TICITICITICITICITICITICI TICITICITICITI		16250	CTCTGTCCT CTCTGTCCT	16340	TCTGTTAGA
Section 178		16240	TGCCTTTCTTTCTTTCTTTCTTCTCTGTCCTTTCTTCTTC		A A C C C A C C C A C C C A C C C A C C C A C C C A C C C A C C C A C C C A C
16140 16150 CITITCITICITICITICI CITITCITICITICITICI			TTTCTTTCT TTTCTTTCT TTTCTTTCT 	16330	TCCTTTAAG TCCTTTAAG TCCTTTAAG TCCTTTAAG
TCTTTT		16230	TGCCTTTC TGCCTTTC	16320	
1613C TCTCTTTC		16220	TTTCTTTG TTTCTTTG TTTCTTTG	16310	O O
16120 TICCTICCI		16210	CTTTCTTCC CTTTCTTCC CTTTTCCTTCC	16300	H H H H H H H H H H H H H H H H H H H
(16108) 16108 16120 16130 SEQ ID NO 1(16108) TCCCTCCCTTCCTTCCTTCTTTCT EQ ID NO 11 (7158) TCCTCCTTCCTTCTTTCT EQ ID NO 12 (200)	558) (1) 367)	(16199) 16199	SEQ ID NO 1(16199) TITICCTTTCTTTCTTTCTTTTTTGEQ ID NO 11 (7249) TITICCTTTCTTTTTTTTTTTTTTTTTTTTTTTTTTTT	(16290) 16290	SEQ ID NO 1(16290) TITCICITIGITITICITICITICC EQ ID NO 11 (7340) TITCICITIGITITICITICITICC EQ ID NO 13 (306)
(16108) 16108 16120 16130 SEQ ID NO 1(16108) TCCTTCCTTCTTTTTTTTTTTTTTTTTTTTTTTTTTT	SEQ ID NO 15 (558) SEQ ID NO 16 (1) SEQ ID NO 17 (367) Consensus(16108)	(161	SEQ ID NO 11 (7249) TITCCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTCTTCT	(162	SEQ ID NO 1(16290) TITCICITIGITITICITICITICCT SEQ ID NO 11 (7340) TITCICITIGITITICITICITICCT SEQ ID NO 13 (306)

Section 181 16471	CCAGGCCT CCAGGCCT CCAGGCCT CCAGGCCT CCAGGCCT CCAGGCCT CCAGGCCT	16562	AATCAGAA AATCAGAA AATCAGAA Section 183 16653 TTACACCC TTACACCC	7774741
S 16460	TTTCATATCTCCAGGCCT	16550	GTGAAGAAA GTGAAGAAA GTGAAGAAA GTGAAGAAA GTGAAGAAA TGCTCATCT TGCTCATCT	101401091
16450	TTTACAGTT TTTACAGTT	16540	######################################	
16440	SEQ ID NO 1 (16381) AGGAAAGTGAAGCACAATTATCAAGGGTCTCCAGTCATCTTCTTTATATCTTTTTACAGTTTCTTCAGGCCTTCAGGCCTTCAGGCCTTCAGGCCTTCAGGAAGTGAAGCACAATTATCTTCTTTTACAGGTTTCAGGCCTTCAGGCCTTCAGGCCTTCAGGAAGTGAAGCACAATTATCTTCAGGAAGCACAATTATCTTCAGGAAGCACAATTATCTTCAGGAAGCACAATTATCTTCAGGAAGCACAATTATCTTCAGGAAGCACAATTATCTCAGGCCTTCAGGAAGCAAATTATCAAATTATCTCAGGGCCTTCAGGAAGCAAATTATCTCAGGAAGCAAAAAAAA	16530	EQ ID NO 11 (7522) TICATIOGGETCAGGATTICGGTGGCCCTTTATGTGTGACAAGTGAAATTAGGGAAAAAAAA	T ぜつりせつつつつり
16430	GTTCTTAATC GTTCTTAATC 	16520	AGTGAAAATA AGTGAAAATA AGTGAAAATA AGTGAAAATA GCCTCATCAA GCCTCATCAA GCCTCATCAA	4401401009
16420	ATCTCCACAT	16510	6161616868 6161616868 6161616868 6161616868 6161616868 040416800 0404168661 0404168661 0404168661	1004014040
16410	STCTCCAGTCCCAGTCCAGTCCCAGTCCCAGTCCCAGTCCCAGTCCCAGTCCCAGTCCCAGTCCCAGTCCCAGTCCCAGTCCCAGTCCCAGTCCCAGTCCCAGTCCCAGTCCCAGTCCCAGTCAGT	16500	16CCCTTTAT 16CCCTTTAT 16S90 AGCTGCTTCC AGCTGCTTCC AGCTGCTTCC AGCTGCTTCC))
16400	ATTATCAAGGCATTATCAAGGCCATTATCAAGGCCATTATCAAGGCCATTATCAAGGCCATTATCAAGGCCATTATCAAGGCCATTATCAAGGCCATTATCAAGGCCATTATCAAGGCCATTATCAAGGCCATTATCAAGGCCATTATCAAGGCAAGGCAAGAAG	16490	16580	70 7 7 7 90997
16390	GTGAAGCACA GTGAAGCACA 	16480	DID NO 11 (7522) TICATIGGGGTCAGGTTGGCATITCG DID NO 15 (558)	
(16381) 16381	3381) AGGAAA(7431) AGGAAA(306)(558)(367)(367)3381)	(16472) 16472	(1522) ITCATT (1522) ITCATT (153) (16472) ITCATT (16563) ICTATT (16563) ICTATT (16663) ICTATT (16663) ICTATT (16663) ICTATT (16663) ICTATT (16663) ICTATTT (16663) ICTATTT (16663) ICTATTT (16663) ICTATTT (16663) ICTATTTT (16663) ICTATTTT (16663) ICTATTTTT (16663) ICTATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	707) ICT GCG
(15)	SEQ ID NO 1 (16381) AGGAAAGTGAAGCACAATTATCAAGGGTCTCCAGTCATCTCCACATGT SEQ ID NO 11 (7431) AGGAAAGTGAAGCACAATTATCAAGGGTCTCCAGTCATCTCCACATGT SEQ ID NO 13 (306)	(16	SEQ ID NO 11 (7522) STOATTGGGTCAGGTTGGCATTTCG SEQ ID NO 13 (306)	O I)eneripellOO

Section 184 15744	TACAAGAA TACAAGAA 	Section 185 16835 CAAGAATG CAAGAATG	CAAGAATG Section 186 CACCTCTC
16730	SEQ ID NO 1(16654) TGTGTGCATGACGAGGCCCACCATTCATTTATCAGAGCCAAAGGCTCTCCCACTATTCTGGTTCACCCCCTAGTTAGCCAGGTATACAAGAA SEQ ID NO 11 (7704) IGTGTGCATGACGAGGCTCACTTTATCAGGCAAAAGGCTCTCCCACTATTCTGGTTCACCTCCTACTTAGCCAGGTATACAAGAA SEQ ID NO 13 (306)	SEQ ID NO 1(16745) 16725 16760 16770 16780 16780 16890 16810 16820 16835 SEQ ID NO 1(16745) TATCTGCACGCATGACTCACCTGCGCACCTCACGCACCTCAGGACTCAGGATTCCATTACTATCGCACCAAGGACAGGATCTCCCAGGAAGAATG SEQ ID NO 11 (7795) TATCTGCACGCATGACTCACCTGGGAGCTCAGAGCTCAGATTCCATTACTATCGCACCAAGGACAGATCTCCCAGGAAGAATG SEQ ID NO 15 (558)	SEQ ID NO 17 (367)
16720	CCCCCCTACT CCCCCCTACT CCCCCCCTACT CCCCCCCTACT CCCCCCCTACT CCCCCCCTACT CCCCCCCTACT CCCCCCCC	16810 ACCAAGGACA ACCAAGGACA ACCAAGGACA	ACCAAGGACA 16900 GAAACCAGAA GAAACCAGAA GAAACCAGAA
16710	TTCTGGTTCA TTCTGGTTCA TTCTGGTTCA	16800 TTACTATCGC TTACTATCGC	TTACTATCGC 16890 ATTCTCCCAA ATTCTCCCAA ATTCTCCCAA
16700	TCTCCCACTA TCTCCCACTA TCTCCCACTA	16790 TCAGATICCA TCAGATICCA TCAGATICCA	1CAGATICCA 16880 AGTICTCTTA AGTICTCTTA AGTICTCTTA
16690	GAGCAAAGGC GAGCAAAGGC GAGCAAAGGC GAGCAAAGGC GAGCAAAGGC	16780 TCAGAGGAGC TCAGAGGAGC 	1CAGAGGAGC 16870 1CCAAAACAC 1CCAAAACAC 1CCAAAACAC
16680	TCATTTATCA TCATTTATCA 	16770 ACCTGGGAGG ACCTGGGAGG	ACCIGGGAGC 16860 AAATCICCCI AAATCICCCI AAATCICCCI
16670	SEQ ID NO 1(16654) TGTGTGCATGACAGGCCCACCATTCEQ ID NO 11 (7704) TGTGTGCATGACAGGCCCACCATTCEQ ID NO 13 (306)	(16745) 16745 16750 16760 16760 SEQ ID NO 1(16745) TATCTGCACGGATGACCTGCCTCACGO ID NO 11 (7795) TATCTGCACGGATGACCTGCCTCACGO ID NO 13 (306)	EQ ID NO 17 (367)
16660	TGCATGACAG TGCATGACAG TGCATGACAG	16750 TGCACGGATG TGCACGGATG	TGCACGGATGAC AAAAGACTAACT AAAAGACTAACT AAAAGACTAACT AAAAGACTAACT
(16654) 16654	SEQ ID NO 1(16654) TGTGT SEQ ID NO 11 (7704) TGTGT SEQ ID NO 13 (306) SEQ ID NO 15 (558) SEQ ID NO 15 (201) TGTGT SEQ ID NO 16 (201) TGTGT SEQ ID NO 17 (367)	SEQ ID NO 1(16745) 16745 16750 SEQ ID NO 1(16745) TATCTGGAG SEQ ID NO 11 (7795) TATCTGGAG SEQ ID NO 13 (306) SEQ ID NO 15 (558) SEQ ID NO 16 (292) TATCTGGAG	7 (367) 8(16745) TATCTGCAC (16836) ACGAAAAG (17886) ACGAAAAG
	SEQ ID NO 1(1 SEQ ID NO 11 (SEQ ID NO 13 SEQ ID NO 15 SEQ ID NO 16 SEQ ID NO 16 SEQ ID NO 16	SEQ ID NO 1(1) SEQ ID NO 1(1) SEQ ID NO 13 SEQ ID NO 15 SEQ ID NO 15 SEQ ID NO 16	SEQ ID NO 17 Consensus(1 SEQ ID NO 1(1 SEQ ID NO 11 (SEQ ID NO 13 SEQ ID NO 13 SEQ ID NO 15 SEQ ID NO 16 SEQ ID NO 16

Section 187 16950 16960 16970 16980 16990 17000 17017	GACCITGABARCAACHGGCCCAITICAGCTATTIAAATCAACTITAAAATCCAACCGCCAAAATTAAAATTAAACCATTITGGTIGGAATG Gaccigaaaacaactggccatitcagctattaaatcaactitaaaatccaactggccaaaatattaaaatg		GACCTGAAAACAACTGGCCATTTCAGCTATTTAAATCAACTTTAAAAATCCAACCGCCAAAATATTAAAATTGGTTGG	17030 17040 17050 17060 17060 17090 17090	CATAACTAACTGGTGACAGGTGCTTGTGGTAGGTGCAAAATGGAAAAAAAA	tgcitcigctaggtgcaaaaatggaaaaaaaaaatacitctaatcaggtcaaatcagttagg	CATAACTAACCTGCTGACAGCTGCTTCTGCTAGGTGCAAAAATGGAAAAAAAA	17120 17130 17140 17150 17160 17170 17180 17199	SEQ ID NO 1(17109) GGATTCTAAATTTACTCATATTCTCAAAGAAATATTCAGTCATAGTGGGGGAAAATAGGATTATTCCTTTAGCTCGATAAGGAACCAGAA SEQ ID NO 11 (8159) GGATTCTAAATTTACTCATATTCTCAAAGAAATATTCAGTCATAGTGGGGGAAAATAGGATTATTCCTTTAGCTCGATAAGCAACCAGAA SEQ ID NO 13 (306)	CTAAATTTACTCATATTCTCAAAGAAATATATTCAGTCATAGTGGGGAAAATAGGATTATTCCTTTAGCTCGATAAGCAACCA	
16940 (1695)	GGACCTGAAAACAACTGGCCAT GGACCTGAAAACAACTGGCCAT	GOACCIGAAAACAACIGGCCAI	TGAAACAACIGGCCAII	8 17030 17040	ATAACTAACCTGCTGACAGC ATAACTAACCTGCTGACAGC	ACATAACTAACCTGCTGACAGCT	ACATAACTAACCTGCTGACAGC	17120	SEQ ID NO 1(17109) GGATTCTAAATTTACTCATATTCTCA EQ ID NO 11 (8159) GGATTCTAAATTTACTCATATTCTCA EQ ID NO 13 (306)	CTAAATTTACTCATATTCTC	
(16927)	GEQ ID NO 1(16927) TAAGGACCC Q ID NO 11 (7977) TAAGGACCCC Q ID NO 13 (306)	SEQ ID NO 15 (558) SEQ ID NO 16 (474) TAAGGACC	Consensus(16927) TAAGGACCC	(17018) 17018	SEQ ID NO 1(17018) ATAMONTAR SEQ ID NO 11 (8068) ATAMONTAR SEQ ID NO 13 (306) SEO ID NO 15 (558)	SEQ ID NO 16 (565) ATRACATA!	Consensus(17018) ATAACATAA	(17109) 17109	SEQ ID NO 1(17109) GGATTCTA/ SEQ ID NO 11 (8159) GGATTCTA/ SEQ ID NO 13 (306)	SEQ ID NO 16 (656) SGATTCTA/ SEQ ID NO 17 (967)	Consensus(17109) GGATTCTAP

17290	ATTTT ATTTT 	SGATTITI GGATTITI Section 191	17381	H	CICIGCCI Section 192	17472	FGTGGC	
17280	300TGAA66/	300TGAASGA 300TGAAGGA Seo	17370		ITCCCACCTO	17460	OTTITE TITE A T T T T T T T T T T T T T T T T T T	
17270	GCTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTTCTT	GCTAICICT GCIAICICT	17360	ACTGACCAA ACTGACCAA 	ACTGACCAA	17450	ATTAAGCAT(ATLAAGCAT(
17260	TCAATCAGAAATTGATTTTTGGAAAACTGTTTCCTATGAAGCTATCTCTGCCTGAAGGATTTTT TCAATCAGAAATTGATTTTTGGAAAACTGTTTCCTATGAAGCTATCTCTGCCTGAAGGATTTTT 	TCAATCASAAATTGATTTTISGAAAACTGTTTCCTATGAAGCTAICTCTGCCTGAAGGATTITT 	17350	AITCACAACCIGGACTITCACCICCAIIGGICAGAGIIITACIGACCAATICCCACCICIGCCI AITCACAACCIGGACIIICACICCAIIGGICAGAGIIIIACIGACCAAIICCCACCICIGCCI	TICACAACCIGGACITICACCICCATIGGICAGAGITITACIGACCAAITCCCACCICIGCCI — Section 192	17440	TICICIICACATACCCCAACAGITACAAAIGGTIGIIAITATTAAGCATCTITTATTTGIGGC TICICIICACATACCCCAACAGITACAAAIGGITGITATTATTATTATGIGGC TICICIICACATACCCCAACAGITACAAAIGGITGITATTATTAAAAGCATCTITTATTTGIGGC	CICIICACAIACCCCGACAGILACAAA1661IGILAIIAAIAA66A1CIIIIAII
17250	668888CT6T	GGAAAACTGT GGAAAACTGT	17340	00750ATTGG 00700ATTGG 10710ATTGG	CCICCAIIGG	17430	AGTTACAAAT	AGT : ACAAA :
17240	ATTGATTTT ATTGATTTTT 	ATTGATTTT ATTGATTTTT	17330	TGGACTITCA TGGACTITCA TGGACTITCA	TGGACTITCA	17420	ATACCCCAAC	ATACCCCAAC
17230		H I H	17320		<	17410		- I
17220		TGACATTEAA TGACATTTAA	17310		ATAGAAGGAA	17400	TATGOOTGTT 1 A 1 G C C T G T T 1	F
17210	SEQ ID NO 1(17200) GITCTICCTICAAATCITGACAITTAA SEQ ID NO 11 (8250) GITCITCCITCAAATCITGACATITAA SEQ ID NO 13 (306)	DID NO 16 (747) SITCTICCTICAAATCITGACATITAA DID NO 17 (367)	17300	SEQ ID NO 1(17291) CITTIACAAICCAGACIAIAGAAGGAA SEQ ID NO 11 (8341) CITIIACAAICCAGACIAIAGAAGGAA SEQ ID NO 13 (306)	Consensus(17291) CITITACAAICCAGACTAIAGAAGGAA	17390	SEQ ID NO 1(17382) TACACCTAACGGAAGITTAIGCCIGIT SEQ ID NO 11 (8432) TACACCTAACGGAAGITTAIGCCIGIT SEQ ID NO 13 (306)	(929) IBCBCCIBACGBAAGIIIAIGCCIGII (387)
(17200) 17200	7200) GIFCTIC 8250) GITCTIC (306) (558)	(747) GITCTEC: (367)	(17291) 17291	7291) CITITACO (306) (558) (838) CITITACO (367)	91) CITITAC.	(17382) 17382	7382) TACACCT. 8432) TACACCT. (306) (558)	(367)
(1720	1 - 50		(1729	NO 1(172) NO 11 (83- NO 13 (34) NO 15 (54) NO 16 (84)	ensus(172)	(173	NO 1(173) NO 11 (84) NO 13 (3(NO 15 (5)	
	SEQ ID NO 1(1 SEQ ID NO 11 SEQ ID NO 13 SEQ ID NO 15	SEQ ID NO 16 SEQ ID NO 17 Consensus(1		SEQ ID NO 1(1) SEQ ID NO 11 (SEQ ID NO 13 SEQ ID NO 13 SEQ ID NO 15 SEQ ID NO 16	Cons		SEQ ID NO 1(1) SEQ ID NO 11 (SEQ ID NO 13 SEQ ID NO 15	SEC ID NO 16

Section 193 17563	GTGTCAA GTGTCAA 	TGTGTCAA IGTGTCAA	17654	TOTOCOR		TTCTCCCA Section 195	17745	ACGAATT ACGAATT	acgaatt	 ACGAATT
S 17550	TIGACCTAATCACAAAAGATIGGTAAAATITCTTAACATATTAATAATATTIGTITATGTGTCTAA TIGACCTAATCACAAAAGATIGGGAAAATITCTTAACATATTAATATITIGTTTTATGIGTCAA 	TIGACCIAAICACAAAAGATIGGIAAAAITICTIAACAIATIAAIAAITITIGIIIAIGIGICAA 	17640	TAACGIICTCTTTITGAAAGAGAATATTAGGATTCAGAGATATTAAGAGATTCICCCA TAACGIICTCTTTITGAAAGAGAATATTAGGATTCAGAGATATTAAGAGATTCTCCCA		GAGGICTTAACGTICTCTTTTGAAAGAGAATATTAGGATTCAGAGATATTAAGGATTCTCCCA Section 195	17730	GATITIAGICCAGGICIGICIACAGCICIAACGIAIAIACACCIIIIGIATAAOAIGICACGAAII GAIITIAGICCAGGICIGICIACAGCICIAACGIAIAIACACCIIIIGIAIAAACAICICAGGAAII 	 8208	
17540	ATTAATAATA ATTAATAATA	ATTAATAAT? ATTAATAATA	17630	ATTCAGAGAT		ATTCAGAGAI	17720	CACCCTTG		CACCCTTTGI
17530	TTCTTAACAT	TTCTTAACAI TTCTTAACAI	17620	GAATATTAGG		GAATATTAGG	17710	AACGTATATA AACGTATATA	.aacgtatat	AACGTATATA
17520	TTGGTAAAAT TTGGTAAAAT	TTGGTAAAA TTGGTAAAA	17610	TTITGAAGA TTITGAAAGA	TTTTGAAAGA	TITIGAAAGA	17700	CTACAGCTCT CTACAGCTCT	CIACAGCICI	CTACAGCICI
17510	TCACAAAAGA TCACAAAAGA	TCACAAAAGA TCACAAAAGA	17600	AACGIICICI AACGIICICI	AACGTTCTCT	AACGIICICI	17690	CCASSTOTST CCASSTOTST 	CCAGGTCTGT	CCAGGTCTGT
17500	6 3-3	E-3 [-1	17590	CAGAGGICII		⊲'.	17580	GGATITIAGI GGATITIAGI 	GGATTTAGT	 GGATTTTAGT
17490	TCCCCTAAAT TCCCCTAAAT	TCCCCTAAAT TCCCCTAAAT	17580	TCAATTAAGAC TCAATTAAGAC		TCAATTAAGA	17670	TAACAGAGCT TAACAGAGCT 	77. 2. 2. 2. 2. 2. 3. 3. 3. 3. 3. 3. 3. 3. 3. 3. 3. 3. 3.	 TAACAGAGCT
17480	SATTACATGG	SATTACATGG SATTACATGG	17570	TAGCATGTA TAGCATGTA		ITAGCATGTA	17660	CACAGITAGG CACAGITAGG 	 cacacatas	 CACAGTTAGG
(17473) 17473	SEQ ID NO 1(17473) CICTGATTACATGGTCCCCTAAATT SEQ ID NO 11 (8523) CICTGATTACATGGTCCCCTAAATT SEQ ID NO 13 (306)SEQ ID NO 15 (558)	SEQ ID NO 16 (1020) CICTGATTACATGGTCCCCTAAATT SEQ ID NO 17 (367)	(17564) 17564 17570	SEQ ID NO 1(17564) TATCTTAGCATGTATCAALTAAGACAGAGGTCTTAACGTTCTTTTTGAAAGAGAGATATTAGGATTCAGAGATATTAAGAGATTCTCCCA SEQ ID NO 11 (8614) TATCTTAGCATGTATCAALTAAGACAGAGGTCTTAACGTTCTTTTTGAAAGAGAATATTAGGATTCAGAGATATTAAGAGATTCTCCCA SEO ID NO 13 (206)	SEQ ID NO 15 (558)	Consensus(17564) TATCTTAGCATGTATCAATTAAGAC	(17655) 17655 17660	SEQ ID NO 1(17655) GGATCACAGITAGGIAACAGAGCIG SEQ ID NO 11 (8705) GGATCACAGITAGGIAACAGAGCIG SEQ ID NO 13 (806)	SEQ ID NO 15 (320)	OND NO N. (307)
	SEQ ID NO 1(17473) SEQ ID NO 11 (8523) SEQ ID NO 13 (306) SEQ ID NO 15 (558)	SEQ ID NO 16 (1020) SEQ ID NO 17 (367) Consensus(17473)		SEQ ID NO SEQ ID NO	SEQ ID NO SEQ ID NO SEQ ID NO	Consen		SEQ ID NO 1(1765) SEQ ID NO 11 (8705) SEQ ID NO 13 (306)	SEQ ID NO	Section No.

(17746) 17746	(17746) 17746 17760 17770 17780 17790 17800 17810 17820 17836	17770	17780	17790	17800	17810	17820	17836
SEQ ID NO 1(17746) こねらこね SEQ ID NO 11(8796)ことらこね SEO ID NO 13 (306)	SEQ ID NO 1(17746) CAGCATAAAGGGATCTTCAGTGATC SEQ ID NO 11 (8796) CAGCATAAAGGGATCTTCAGTGATC SEO ID NO 13 (306)	GTGATCTAAGT GTGATCTAAGT 	O A G G G G T C A G G G G G T C A G G G G G T C A G G G G T C A G G G T C A G T C A G T	CAACCTTTTC CAACCTTTTC 	TAAAAAGGAC(TaaaaaggaC(3&&&	TAAGTCAGGGGTCAGCAACCTTTTCTAAAAGGACCAAATAGTAATATTTTCAGGGTTTGTGGACCCC TAAGTCAGGGGTCAGCAACCTTTTCTAAAAGGACCAAATAGTAATATTTCAGGGTTTGTGGACCC	#6#66ACCC #6#66ACCC
(558) 1293) : ^	SEQ ID NO 15 (558)	1	AAGTCAGGGGTCAGCAACCITI	CAACCTITIC			TCTAAAAAGGACCAAATAGTAATATTTCAGGCTT	1 9 9 E 9 E 9 E 9 E 9 E 9 E 9 E 9 E 9 E
(367) 7746) CAGCA	JID NO 17 (367)	GTGATCTAAGT	CAGGGGTCAG	CAACCITITC	TAAAAAGGAC	CAAATAGTAA	TAAGICAGGGGICAGCAACCITITCTAAAAGGACCAAATAGIAATATITCAGGCTTTGIGGACCC Section 197	TGTGGACCC Section 197
(17837) 17837	17850	17860	17870	17880	17890	17900	17910	17927
SEQ ID NO 1(17837) IMTIGE SEQ ID NO 11 (8887) FARIGE SEQ ID NO 13 (306) SEQ ID NO 15 (558)	SEQ ID NO 1(17837) TATGGTCTCTATCATAACTGTTCAAATCACCATGTAGTGTAAAAGGAGCCATAAGCAAAATATAAACTAACGAATGTGGGTG SEQ ID NO 11 (8887) TATGGTCTCTATCATAACTGTTCAAATCACCATGAAAAGGAGCCATAAGCAAAATATAAACTAACGAATGTGGCTG SEQ ID NO 13 (306)	GITCAAAICAC GITCAAAICAC 	CATGEAGT GT	AAAAGGAGCC AAAAGGAGCC 	ATAAGCAAAA ATAAGCAAAA 	TATAAKTAA EATAAAKTAA	AICACCAIGIAGIGIAAAAGGAGCCAIAAGCAAAIMIAAACIAACGAAIGIGGGIGIIITAIGGG AICACCAIGIAGIGIAAAAGGAGCCAIAAGCAAAAIAIAAACIAACGAAIGIGGCIGIIIIAIGGG 	12TTATGGG
384) TAIGG	SEQ ID NO 16 (382) SEQ ID NO 16 (382) SECTIONAL CATARCTETICAL SECTIONAL CONTRACTOR CONTR	12	CAIGTAGIGI	AAAAGGAGCC	ATAAGCAAAA	ERTRABCIAS	tcaccatgtagtgtaaaaggagccataagcaaaatataaactaacgaatgtggttttatggg	TITIATGGG
(307) 7837) TATGG	Consensus(17837) TAIGGICICIAICAIAACIGIICAA	ı ⊲C l	CATGTAGTGT	AAAAGGAGCC	ATAAGCAAAA	 FATAAACTAA	TCACCATGTAGTGTAAAAGGAGCCATAAGCAAAATATAAACTAACGAATGTGGCTGTTTTATGGG Section 198	TITIAIGGG — Section 198
(17928) 17928	17940	17950	17960	17970	17980	17990	18000	18018
SEQ ID NO 1(17928) ATTITE SEQ ID NO 11 (8978) ATTITE SEQ ID NO 13 (306)	SEQ ID NO 1(17928) ATTITITITAACTCTITATACAAAAGCAGGTGGCAGATCAGAACTCACTTATGGGCCATAGTTCTCTGACCCCTGACCTGAAAAATC SEQ ID NO 11 (8978) ATTITITITAACTCTTTATTTACAAAAGCAGGTGGCAGATCAGAACTCACTTATGGGCCATAGTTCTCTGACCCCTGACAAAATC SEQ ID NO 13 (306)	TTTACAAAAGC TTTACAAAAGC	AGGTGGCAGA AGGTGGCAGA	TCAGAACICA TCAGAACICA 	CTTATGGGCC CTTATGGGCC	ATAGITCICI ATAGITCICI	AAAGCAGGIGGCAGAICAGAACICACIIATGGGCCAIAGIICICICIGACCCCTGACCIGAGAAAAIC AAAGCAGGIGGCAGAICAGAACICACIIAIGGGCCAIAGIICICIGACCCTGACCIGAGAAAAIC 	GAGAAATC GAGAAAATC
(558) 1475) ATTIT	SEQ ID NO 15 (558)SEQ ID NO 16 (1475) AITITITITITIACA	TITACAAAAGC	 aggtegtara	TORGRACTCR	CITAIGGGCC		 aaagcagsisgcabatcagaactcactiaigggccaiagiicicigacccigacciga	GAGAAAATC
(367) 7928) ATITI	JID NO 1/ (367)	75444474TT	454755F554	47 L 7 4 4 5 4 7 L				GAGAAAATC

18109	6 A A A G C A 6 A A A G C A 	GAAAGCA GAAAGCA	ecilon	GACTCCT GACTCCT 	GACTCCT	GACTCCT	18291	TCTTATC ICTTATC	TCITAIC	TCTTATC
	004011 04011 1 1 01101	SEMETICE 	18190	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	 GACCATA	GACCATA	18280	TOCATT		TCCATT
18090	31CAAGGCTG	STCAAGGCTG STCAAGGCTG	18180	VAAGAATAAT VAAGAATAAT	 \A&G&AT&&T	AAAGAATAAT	18270	CTCCAGGCC	 ICICCAGGCC	ICTCCAGGCC
18080	CAACTGAAGC	CAACTGAAGC CAACTGAAGC	18170	AAGAAGCACA AAGAAGCACA	 aagaagcacz	AAGAAGCAC <i>i</i>	18260	TACCTAATCI TACCTAATCI	TACCIAAIC	 TACCTAATC1
18070	AAGCTCTGT AAGCTCTGT 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	AAGCTCTGT	18160	CCCAGITAT CCCAGITAT		CCCAGTTAT	18250	AGGCCAAGT AGGCCAAGT	AGGCCAAGT	AGGCCAAGT
18060	TAAGAACAAG TAAGAACAAG 	TAAGAACAAG TAAGAACAAG	18150	GIINGAAGAI GIIAGAAGAI		GTTAGAAGAT	18240	TGTATGGTCC TGTATGGTCC	TGIATGGICC	TGTATGGTCC
18050	ACTTGCCAAG ACTTGCCAAG	ACTIGCCAAG ACTIGCCAAG	18140	AATAGITAAA AATAGITAAA 		AATAGTTAAA	18230	GCACTCTTGT	1-4	
18040		() 1 ()	18130	TGATAAGIGA FGATAAGIGA	 TGATAAGTGA	(י)	18220	TCTGGCTTAG TCTGGCTTAG	F-4	Ι [
18030	TGGACAACAT TGGACAACAT	TGGACAACAT TGGACAACAT	18120	CIGGIGILAA CIGGIGILAA 	 CIGGIGILAA	CTGGTGTTAA	18210	TGTCTGGACT TGTCTGGACT	TGTCTGGACT	TGTCTGGACT
1) 18019) TIATATITA)) TIATATITA))) TTATATTTA))) TTATATTTA	0 18110) AAGAGCIGI) AAGAGCIGI)	3) 7) AAGAGETET 7)) AAGAGCTGT) GAACAAGAA) GAACAAGAA))))GAACAAGAA
(18019	EQ ID NO 1(18019 Q ID NO 11 (9069 Q ID NO 13 (306 Q ID NO 15 (558	Q ID NO 16 (1566 Q ID NO 17 (367 Consensus(18019	(18110	EQ ID NO 1(18110 Q ID NO 11 (9160 Q ID NO 13 (306	2 ID NO 15 (558 2 ID NO 16 (1657 10 NO 17 (367	Consensus(18110	(18201	CO ID NO 1(18201 CO ID NO 11 (9251 CO ID NO 13 (306	2 ID NO 16 (1748	JID NO 1/ (367)
	18040 18050 18060 18070 18080 18090	3019) 18019 18050 <th< td=""><td> 18050</td><td>18050 18050 18060 18070 18080 TGTGACTTGCCAAGTAAGAACAAGAAGCTCTGTCAACTGAAGGT </td><td> 18050 18060 18070 18080 18080 18080 18080 18080 18080 18080 18080 18080 18080 18080 18080 18080 18170 18160 18170 18160 18170 18160 18170 18160 18170 18160 18170 18160 18170 18160 18170 18160 18170 18160 18170 18160 18170 18160 18170 18160 18170 18160 18170 18160 18170 18160 18170 18170 18160 18170 18160 18170 18160 18170 18160 18170 18160 18170 18160 18170 18160 18170 18160 18170 18160 18170 18160 18170 18160 18170 18160 1817</td><td> 18050 18060 18070 18080 18080 18080 18080 18080 18080 18080 18080 18080 18080 18080 18080 1808 18080 18150 18150 18160 18170 18170</td><td> 18050 18060 18070 1808</td><td> 18050 18060 18070 18080 18080 18050 18080 18050 18050 18050 18050 18050 18050 18050 18050 18050 18050 18050 1825</td><td> 18050 18060 18070 18080 18050 18050 18050 18050 18050 18050 18050 18050 18050 18050 18170 18150 18170 18150 18170 18150 18170 18150 18170 18150 18170 18150 18170 18150 18170 18150 18170 18150 18150 18170 1815</td><td> 18050 18060 18070 18080 </td></th<>	18050	18050 18050 18060 18070 18080 TGTGACTTGCCAAGTAAGAACAAGAAGCTCTGTCAACTGAAGGT	18050 18060 18070 18080 18080 18080 18080 18080 18080 18080 18080 18080 18080 18080 18080 18080 18170 18160 18170 18160 18170 18160 18170 18160 18170 18160 18170 18160 18170 18160 18170 18160 18170 18160 18170 18160 18170 18160 18170 18160 18170 18160 18170 18160 18170 18160 18170 18170 18160 18170 18160 18170 18160 18170 18160 18170 18160 18170 18160 18170 18160 18170 18160 18170 18160 18170 18160 18170 18160 18170 18160 1817	18050 18060 18070 18080 18080 18080 18080 18080 18080 18080 18080 18080 18080 18080 18080 1808 18080 18150 18150 18160 18170 18170	18050 18060 18070 1808	18050 18060 18070 18080 18080 18050 18080 18050 18050 18050 18050 18050 18050 18050 18050 18050 18050 18050 1825	18050 18060 18070 18080 18050 18050 18050 18050 18050 18050 18050 18050 18050 18050 18170 18150 18170 18150 18170 18150 18170 18150 18170 18150 18170 18150 18170 18150 18170 18150 18170 18150 18150 18170 1815	18050 18060 18070 18080

SEQ NO 11, 13, 15, 16 and 17 against SEQ NO 1

TCCTCABASASCTGTAAAAAAAAAACTBAACCCAIGTCAAGCACATAGAATAGGSCCCAGCC	TCCTCAGAGAGCTGTAAGAATAACTGAGCTAACCCATGTCAAGCACATAGAATAGGGCCCAGGC TCCTCAGAGAGCTGTAAGAATAACTGAGCTAACCCATGTCAAGCACATAGAATAGGGCCCAGCC TCCTCAGAGAGCTGTAAGAATAAACTGAGCTAACCCATGTCAAGCACATAGAATAGGGCCCAGCC Section 203	TTCCTCAGAGACTGTAAGATAAACTGAGCTAACCCATGTCAAGCACATAGAATAGGGCCCAGCC TTCCTCAGAGAGCTGTAAGAATAAACTGAGCTAACCCATGTCAAGCACATAGAATAGGGCCCAGCC TTCCTCAGAGAGCTGTAAGATAAACTGAGCTAACCCATGTCAAGCACATAGGGCCCAGCC Section 203 18410	TGTCAAGCACATAGAATAGGGCCCAGCC TGTCAAGCACATAGAATAGGGCCCAGCC TGTCAAGCACATAGAATAGGGCCCAGCC 18450	ATGTCAAGCACATAGAATAGGSCCCAGCC ATGTCAAGCACATAGAATAGGSCCCAGCC ATGTCAAGCACATAGAATAGGSCCCAGCC ATGTCAAGCACATAGAATAGGSCCCAGCC ATGTCAAGCACATAGAATAGGSCCCAGCC ATGTCAAATGTTATCTACAGATTGGCATTGT 18450	TICCICAGAGAGCIGIAAGAATAAACTGAGCIAACCCAIGTCAAGCACATAGAATAGGGCCCAGCC TICCICAGAGAGCTGIAAGAATAAACTGAGCTAACCCATGICAAGCACATAGAATAGGGCCCAGCC Section 203 18410 18420 18430 18440 18450 18460 18473 GCTACATATTAGTTCTCTATATTTTTTTTTTTTTTTTTT	TGTCAAGCACATAGAATAGGGCCCAGCC
	FGAGCTAACCCA TGAGCTAACCCA TGAGCTAACCCA	TGAGCIAACCCA TGAGCIAACCCA TGAGCIAACCCA TTCATIATCATA	TGAGCTAACCCA TGAGCTAACCCA TGAGTATATCATA	18530	16AGCTAACCCA 16AGCTAACCCA 18440 ATTCATTATCATA 18530 ATTGATCTGCAT(18530
		STAAGAATAAACT STAAGAATAAACT STAAGAATAAACT SO 18430 CTCTATATTTTTA	STAMGAATAAACT STAAGAATAAACT STAAGAATAAACT CCTATATTTTTA	STANGAATAAACT STAAGAATAAACT STAAGAATAAACT CTCTATATTTTTA CTCTATATTTTTTA CTCTATATTTTTA CTCTATATTTTTA CTCTATATTTTTTA CTCTATATTTTTA CTCTATATTTTTTA CTCTATATTTTTTA CTCTATATTTTTTA CTCTATATTTTTTA CTCTATATTTTTTA CTCTATATTTTTTA CTCTATATTTTTTA CTCTATATTTTTTTA CTCTATATTTTTTTA CTCTATATTTTTTTA CTCTATATTTTTTTT	STAAGAATAAACT STAAGAATAAACT STAAGAATAAACT CTCTATATTTTTA CTCTATATTTTA CTCTATATTTTTA CTCTATATTTTA CTCTATATTTTTA CTCTATATTTTTTA CTCTATATTTTTA CTCTATATTTTTA CTCTATATTTTTTA CTCTATATTTTTTA CTCTATATTTTTTA CTCTATATTTTTTA CTCTATATTTTTTA CTCTATATTTTTTA CTCTATATTTTTTA CTCTATATTTTTTTT	STANGAATAAACT STAAGAATAAACT STAAGAATAAACT CTCTATATTTTTA CTCTATATTTTA CTCTATATTTTA CTCTATATTTTA CTCTATATTTTA CTCTATATTTA CTCTATATTTA CTCTATATTTA CTCTATATTTA CTCTATATTTA CTCTATATTTA CTCTATATTA CTCTATATT
TCCTCAGASCTC	TCCTCAGAGCTC	TCCTCAGAGAGCTGT TCCTCAGAGAGCTGT 18410 18420 CTACATATTAGTTCT	TCCTCAGAGAGCTC TCCTCAGAGAGCTC 18410 1845 CTACATATTAGTTC	TCCTCASASCTC TCCTCASASASCTC TCCTCAGAGAGCTC TACATATTAGTTC	TCCTCAGAGAGCTG TCCTCAGAGAGCTG TCCTCAGAGAGCTG TCTACATATTAGTTC	TCCTCAGAGAGCTC TCCTCAGAGAGGTC 18410 1846 CTACATATTAGTTC
-4	I H	40 I FH 100 (60 I I	字 I 日	S I F4 (100 (0) I I (0) I (0)		
	LAAATGAAGATA.	(18383) 18383 18390 (18383) 1871 AATTAATCA (18383) 1871 AATTTATC (9433) 1871 ATTATC (306)	33 18390 (ATTAATTTATC (ATTAATTTATC (ATTAATTTATC	33 18390 CATTANTTANC CATTANTANTTANC CATTANTANT CATTANT CATTANTANT CATTANT CATTANTANT CATTANTANT CATTANTANT CATTANTANT CATTANTANT CATTANT CATTANTANT CATTANTANT CATTANTANT CATTANTANT CATTANTANT CATTANT C	33 18390 53 18390 54 18480 56ATGAGTTATC 67 17 AATTTATC 67 17 AATTTATC 67 18480 68 18480 69 18480 60 18480	33 18390 (ATTAATTTATC. (ATTAATTTATC. (ATTAATTTATC. (ATTAATTTATC. (ATTAATTTATC. (ATTAATTTATC. (ATTAATTTATC. (ATTAATTTATC.
	Sed ID NO 17 (367)	SEQ ID NO 17 (367)	SEQ ID NO 17 (367)	SEQ ID NO 17 (367) Consensus(18292) ATT (18383) 1838 SEQ ID NO 11 (3433) TAT SEQ ID NO 11 (3433) TAT SEQ ID NO 13 (366) SEQ ID NO 15 (558) SEQ ID NO 16 (1930) TAT SEQ ID NO 17 (367) Consensus(18383) TAT	SEQ ID NO 17 (367)	SEQ ID NO 17 (367) Consensus(18292) ATTA (18383) 18383 SEQ ID NO 1(18383) TATA SEQ ID NO 13 (306) SEQ ID NO 15 (558) SEQ ID NO 16 (1930) TATA SEQ ID NO 17 (367) Consensus(18383) TATA SEQ ID NO 1 (18474) AAGG SEQ ID NO 1 (9459) SEQ ID NO 1 (1956) SEQ ID NO 1 (1956)

SEQ NO 11, 13, 15, 16 and 17 against SEQ NO 1

								Section 205
(18565) 18565 18570	18580	18590	18600	18610	18620	18630	18640	18655
SEQ ID NO 1(18565) GTAACAACATTCATTTTGCAAACAA	ATTCATTTTGCAA?	ACAAATTTGA	AATTTGAGGA	GGGCTTGTCT	GGGAAGACITG	TCTCTGCCC	ATTTGAAATTTGAGGAGGGCTTGTCTGGGAAGACTTGTCTCTGCCCTATGTGGTATCAGCAGGGGG	GCAGGGGG
SEQ ID NO 11 (9459) SEQ ID NO 13 (306)								
SEQ ID NO 15 (558) SEQ ID NO 16 (1956)								
SEQ ID NO 17 (367) Consensus(18565)	 							
								Section 206
(18656) 18656	18670	18680	18690	18700	18710	18720	18730	18746
SEQ ID NO 1(18656) AGGCTTGACGGACTGGCACATGCCCTTCCAGAATGGCCCACTCGCATGCCTGCC	CGGACTGGCACATO	SCCCTTCCAG	AAIGGCCCAC	TCGCATGCCT	GCCAAGIIGGI	GCIGGCICI	TGGCTGGGAGCI	CAGCIGGG
SEQ ID NO 11 (9459) SEQ ID NO 13 (306)								
SEQ ID NO 15 (558)								
SEQ ID NO 16 (1956) SEO ID NO 17 (367)								
Consensus(18656)	 	 	 	 	 	 	 	
								Section 207
(18747) 18747	18760	18770	18780	18790	18800	18810	18820	18837
SEQ ID NO 1(18747) GCIGAGIGCIAGGGICCCIGGGAGG	CIAGGGTCCCTGG	SAGGIICCII	STGGCCTGAA	CITCCICACC	ACAAGGCGGCI	GCGGTGCGA	IICCIIGIGGCCIGAACIICCICACCACAAGGCGGCIGCGGIGCGAGAGIGAGCAIIICAAGAIAG	CAAGATAG
SECTIONO 13 (306)								
SEQ ID NO 15 (558)								1 1 1 1 1 1 1 1 1
SEQ ID NO 16 (1956)								
SEQ ID NO 17 (367)								
Consensus(18747)								

SEQ NO 11, 13, 15, 16 and 17 against SEQ NO 1

SEQ ID NO 11 (9459)									007 1101000	007
SEQ ID NO 1(18838) AGC SEQ ID NO 11 (9459) SEQ ID NO 13 (306)	38	18850	18860	18870	18880	18890	18900	18910		18928
SEO ID NO 13 (306) =	CAAGATG	ACACTGTAT 	TACTGTGTAA	GTAAGACCCAGCCTGGGAATTAATGTAGCCTCACTTCCATCCCACTCTATTTT	GGGAATTAAT	GTAGCCTCA(SITCCAICCC	ACTCTATTTT 	TAAAAGTGAATT 	ATT
SEQ ID NO 15 (558)										
SEQ ID NO 16 (1956)										
Consensus(18838)									:	Ç.
									Section 209	503
(18929) 18929	නු	18940	18950	18960	18970	18980	18990	19000	•	19018
SEQ ID NO 1(18929) ATTAAGGICACCCCATATICAAGGG	AAGGICAG	CCCCATATT	CAAGGGGATA	GGAATTAGAC	TICAICIGIA	TTAAGAAAA	ATGTTTTAA	GATAGGAATTAGACTTCATCTGTATTAAGAAAATGTTTTTAAAAATTGTAGACATGTTTTAAAA	CATGTTTAA	AAT
SEQ ID NO 13 (306)										
SEQ ID NO 15 (558)										
SEQ ID NO 16 (1956)										
SEG ID NO 17 (367) Consensus(18929)	 	 	 	 	 	 	 	 	 	
									Section 210	210
(19020) 19020	03	19030	19040	19050	19060	19070	19080	19090	19100	19110
SEQ ID NO 1(19020) TCTAAAGTCCACTTACTGGCTGCAGATTATTATATACATGCAAGATACACTCCTACATTCTCTTTAGAAGGCTCAGTTGCAGTAC	AAAGTCCA	ACTTACTGG	CIGCAGAITA	TTTATATATA	CATGCAAGAI	ACACTCCTA(CATTCTCTTC	TTAGAAGGCT	CAGIIGCAGG	TAC
SEQ ID NO 11 (9459)										
SEQ ID NO 15 (558)										
SEQ ID NO 16 (1956)			 	 			1 1 1 1 1 1 1	 	 	
SEQ ID NO 17 (367)										
Consensus(19020)										

SEQ NO 11, 13, 15, 16 and 17 against SEQ NO 1

Section 211	ACCTACAT	19292	CAGICAIT	19383	TGCTCTTG
19190	TATTTGCAL	19280	.GCACATAA(19370	TTCCCTAC
19180	AGAGACAAGI	19270	TAAATAGAGGAAAATGAGAGCACATAACAGTCATT	19360	ACTGCCTGGA
19170	TGTAAACTA	19260	ITAAATAGAG	19350	TCTCAGTCCTCAGTCCT
19160	ATCTGAAGAC	19250	CACTCTTGTT	19340	TTTTTAGG
19150	TATCCTCTCA.	19240	CCACTACAGA 	19330	CAAGCAGGTC
19140	TTATGTATT	19230	ATAGGACAG(19320	CAGCAAACACACACACACACACACACACACACACACACA
19130	GTGAGATTT(19220	STAAAGTATA(19310	GATATCCAGA
19120	AGCTCTTCA2	19210	TATICAAIGG	19300	TAGCAACTCT
(19111) 19111	SEQ ID NO 1(1911) SEQ ID NO 11 (9459) 9459) SEQ ID NO 13 (306) 306) SEQ ID NO 15 (558)	(19202) 19202	SEQ ID NO 1(19202) ACGCAATATTCAATGGTAAAGTATACATAGGACAGCCACTACAGACACTCTTGTTT SEQ ID NO 11 (9459)	(19293) 19293	SEQ ID NO 1(19293) GGCTCATAGCAACTCTGATATCCAGACAACCAAAGCAGGTCTTTTTTTT
	SEQ I SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID		SEQ II SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID		SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID Con

SEQ NO 11, 13, 15, 16 and 17 against SEQ NO 1

									Section 214
(19384) 19384	19390	19400	19410	19420	19430	19440	19450	19460	19474
SEQ ID NO 1(19384) GGICTICCCICCAGGIICIIGGIIC	TCCCTCCA	SGTTCTTGGT	: ⊢	CITITCATI	AATACTATT	CIGIICCIII	AAGTICAAG	TGGACCTCTTTTCATTTAATACTATTTCTGTTCCTTTAAGTTCAAGCTGGCAAAATATGATTGTA	ATGATTGTA
SEQ ID NO 13 (306)									
SEQ ID NO 15 (558)									1 1 1 1 1 1 1 1 1 1
SECTION OF (1936) SECTION OF (367)			! ! ! ! ! ! ! ! ! ! ! ! ! !				 		
Consensus(19384)									
									Section 215
(19475) 19475 19480	19480	19490	19500	19510	19520	19530	19540	19550	19565
SEQ ID NO 1(19475) CAATTCTGTTTAAAATTCCAGGACT	CIGITIAA	AATTCCAGGA	CIICCIGIGA	ATICITATIGG	GGAATACTCO	ATTAGACAAG	AATCICIII	TCCTGTGATICTTATTGGGGAATACTCCATTAGACAAGAATCTCTTTGACATAAGCCATTCTCTAC	ATTCTCTAC
SEQ ID NO 11 (9459)					 	 			
SEQ ID NO 13 (306)									
SEC ID NO 15 (558)			 	 	 	 			
SECTIONO 17 (367)									
Consensus(19475)									
									Section 216
(19566) 19566		19580	19590	19600	19610	19620	19630	19640	19656
SEQ ID NO 1(19566) CIGAGAICCCIGIAAGGCIGIGAIG	AICCCIGI	AAGGCTGTGA	TGGGACCACA	ATAACCTTAAA	ATTATTAGAP	GACTCATIGI	TIACIGAGA	GGACCACATAACCTTAAAATTATTAGAAGACTCATTGTTTACTGAGAGAATATGCCTAGCATATGC	AGCATATGC
SEQ ID NO 11 (9459)									
SEQ ID NO 13 (306)				1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1			1 1 1 1 1 1 1 1		
SEQ ID NO 15 (558)									
SEQ ID NO 16 (1956)		1 1 1 1 1 1					1 1 1 1 1 1 1		
SEO ID NO 17 (367)									
Consensus (19566)									
COLINGIA DO COCO									

SEQ NO 11, 13, 15, 16 and 17 against SEQ NO 1

								Section 217
(19657) 19657	19670	19680	19690	19700	19710	19720	19730	19747
SEQ ID NO 1(19657) TIAGATCCTTAGAGGAACTCTGTTT SEO ID NO 11 (19459)	FTAGAGGAACTO	TGTTTCAAA	SGGCTTATGA	SACATTACCT	ratatcitic:	FAAGGTACAA	CAAAGGGCTTATGAGACATTACCTTATATCTTTCTAAGGTACAAACAA	GGCTTTTGA
SEQ ID NO 13 (306) SEQ ID NO 13 (306) SEQ ID NO 15 (558)								
SEQ ID NO 16 (1956) SEQ ID NO 17 (367)								
Consensus(19657)								Section 218
(19748) 19748	19760	19770	19780	19790	19800	19810	19820	19838
SEQ ID NO 1(19748) GITIGAICTITGAGCIGACACCITT	ITTGAGCTGACA	ACCTTTTCT7	AATTTGAGAA	TCTTAATTTGAGAATCCCCTGCTCTATGGAGAGACTGACAAAGAGAAATAGTT	IATGGAGAGA	CTGACAAAGA	SAAATAGTTTAT	TTATATTTGAATG
SEQ ID NO 11 (9459) SEQ ID NO 13 (306)								
SEQ ID NO 15 (558)	! ! ! ! ! ! ! ! ! ! ! ! ! ! ! ! ! ! ! !							
SEQ ID NO 16 (1956) SEQ ID NO 17 (367)								
Consensus(19748)								
				,				Section 219
(19839) 19839	19850	19860	19870	19880	19890	19900	19910	19929
SEQ ID NO 1(19839) TAACATCTTGGATCTTTAATAGATT.	IGGATCTTTAA 1	RAGATTATCT	FAAAATTTTC	ATCTTAAAATTTTCCTGAAAATGTAACAGTTCCT	AACAGIICCI	LTTTTAAAA	TITITIAAAATICATICICCCIACACACTIAI	CACACTTAT
SEQ ID NO 13 (306)								
SEQ ID NO 15 (558)								
SEQ ID NO 16 (1956)								
SEQ ID NO 17 (367)								
Consensus(19839)								

SEQ NO 11, 13, 15, 16 and 17 against SEQ NO 1

							Section 220
(19930) 19930 19940 19950	19940	19950	19960	19970	19980	19999	
SEQ ID NO 1(19930) TATATATGACTAAAAGAAACTCCC	TGACTAAAAGA	AACICCCIGG	CATITICAAC	ATICIGGITA	GAATTTTTCI	TGGCATTTTCAACATTCTGGTTAGAATTTTTCTTAGCCCAATCTAC	
SEQ ID NO 11 (9459)							
SEQ ID NO 13 (306)							
SEQ ID NO 15 (558)							
SEQ ID NO 16 (1956)							
SEQ ID NO 17 (367)							
Consensus(19930)							

EXHIBIT B

align SEQID#2 against SEQID#11.apr

	1	Ç	CC	90	Ç	Cu	C	20	Section 1	on 1
SEQ ID NO 11) ATTIGAATIGGIGAACTIAGIAAAG	CITAGTAAAGCA	SACGGCTCTCA	40 ACCAATAAGG	SCAGGCAICA	TCCAAICIGI	CGAAAGCIIG	CAGACGGCTCTCACCAATAAGGGCAGGGATCATCCAATCTGTCGAAAGCTTGAATAAAAAAAA	AAG
SEQ ID NO 13		 TGAATTGGTGA	 CITAGIAAAGCA	 gacgcicica	 accaataagg	 GCAGGCATCA	TCCAATCTGT	 CGAAAGCTIG		AAG
SEQ ID NO 15 SEQ ID NO 16 SEQ ID NO 17 Consensus										0
	(92) 92	100	110	120	130	140	150	160	170 182	182
SEQ ID NO 11		(92) AGGAAGGGAAATTTGCTTCTTTC	} [─	CITGAICTAGI	ATATCATCT	rcrccrgccc	TIGGATGIGA	GIGGCCCIIC	TCTTGATCTAGTATATCATCTTCTTCTGCCCTTGGATGTGAGTGGGCCTTCAGACTTAAACCAGG	AGG
SEQ ID NO 13		(1)	I ⊟	 CTTGATCTAGI	 [ATATCATCT]	ICICCIGCCC	TIGGAIGIGA	GIGGGCCIIC	 TCTTGATCTAGTATATCATCTTCTCCTGCCCTTGGATGTGAGTGGGGCCTTCAGACTTAAACCAGG	 AGG
SEQ ID NO 16 SEQ ID NO 17										
Consensus	(92)								Section 3	
	(183) 183	190		210 2	520	230	240	250	260	273
SEQ ID NO 11	(183) AGI	TIGGC	ITCCCIGGIICI	CICAGIICIIIGG	SACTIGGACT	GAATTACACT	GCCAGGIIIC	CIGGIICICC	TGGACTTGGACTGAATTACACTGCCAGGTTTCCTGGTTCTCCAGCTTGCAGATGGC	299
SEQ ID NO 13	(183) AGT (183) AGT	TTTGGC	TCT	CAGTICTTIGGA	CITGGAC	TGAATTACACTGCCAG	GTTTC	CIGGIICICC	CCAGCTTGCAGAT(TGGC
SEQ ID NO 16	(f) (f)									
SEQ ID NO 17	(1)									
Consensus (183)	(183)									

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align SEQID#2 against SEQID#11.apr

SEQ ID NO 2	>()	280 CATGGGACT	(274) 274 280 290 SEQ ID NO 11 (274) AGATCATGGGACTTCTTGGCCTCCA	300	310 FGAGTCAATT	320 TCCATTTTAT	330 TTACATATCC	340 GTTATGCAT	350 TGCTTAACAATC	364 364 GACA
1 1 1 1 1 1 1 1 1 1	NO 2 (1) NO 13 (274) AGAT NO 15 (1) NO 16 (1)	CATGGGACT CATGGGACT		D - - - - - - - - -	-	-		-		4
(365) 365 370 380 490 410 420 430 440 (365) GGTTCTGAGAATGCATTGTTAAGTGATTTCATCATTGTGCAAACATCATAGAGTGTAACTACACAACCTGGACAGCATAGACTACTACTACTACTACTACTACACAAACCTGGACAGCATAGACTACTACTACTACTACTACTACTACTACTACTACTACTA	•									 - Section 5
(1)	(365) 365 NO 11 (365) GGII	370 CIGAGAAAT	380 GCATIGITAA	390 GIGATITCATO	400 CATIGIGCAA	410 ACATCATAGA	420 STGTAACTACA	430 CAAACCIGG	440 ACAGCATAGACI	455 ACTACA
(1)	NO 13 (306) NO 15 (1)									
(456) 456 470 480 490 500 510 520 530 546	. ლ									Section 6
	(456) 456		470	480	490	500	510	520	530	546
	NO 15 (1)	 								
NO 15 (1)	SECTIONO 16 (1) SECTIONO 17 (1)									
2	Consensus (456)									

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align SEQID#2 against SEQID#11.apr

	(547) 547	560	570	580	590	009	610	620	Section 7 637
SEQ ID NO 11 (547) AAA. SEQ ID NO 2 (1) SEQ ID NO 13 (306) SEQ ID NO 15 (1) SEQ ID NO 16 (1) SEQ ID NO 17 (1) Consensus (547)	SEQ ID NO 11 (547) AAAAGGTACAGTAAAAATATGGTAT SEQ ID NO 2 (1)	GTAAAATAT GTAAAATAT GTAAAATAT GTAAAATAT	GGTATAATCT	TATGGGATCAC	CATCATATAC	IGCAATCCTT	TGTAGACTG.	AATCTTATGGGATCACCATCATATATGCAATCCTTTGTAGACTGAAATGTCATTGTGTGTG	TGCATG
	(638) 638	650	099	670	680	069	700	710	728
SEQ ID NO 11 (638) SEQ ID NO 2 (1) SEQ ID NO 13 (306) SEQ ID NO 15 (1) SEQ ID NO 16 (1) SEQ ID NO 16 (1) SEQ ID NO 17 (1) Consensus (638)	(638) ACTGTATACG (1) (306) (1) (1) (1) (638)	CACACATACA(CAAACACACACACACACACACACACACACACACACACA	CAAATATACTA 	NTGGTTCTTT	TTCTCTGAA	GAGCCCTAA	TTCTCTGAAGAGCCCTAATACAATATGTTATACATTTATA	TTTATA
	562 (562)	740	750	760	770	780	062	800	Section 9
SEQ ID NO 11 (729) TTG. SEQ ID NO 2 (1) SEQ ID NO 13 (306) SEQ ID NO 15 (1) SEQ ID NO 16 (1) SEQ ID NO 17 (1)	SEQ ID NO 11 (729) TTGACTCTATTTCAAAATTTATGGT SEQ ID NO 2 (1)	TTCAAAATTT.	ATGGTTTTGG	TGAAACATATG	STGGAGATGG(GGCATAGGTG	TGTGAACTG	TTTGGTGAAACATATGTGGAGATGGGGCATAGGTGTGTAACTGGGATAGTGTCCTGCTGATGAAT	ATGAAT
Consensus (729)	(729)								

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Section 10 (820) 820 830 840 850 860 870 880 890 910 910 SEO 10 NO 11 (820) 820 830 830 840 850 850 810	830	840	850	860	870	880	890 TATTTOADD	006	Section 10 910
SEQ ID NO 13 (306) SEQ ID NO 13 (306) SEQ ID NO 15 (1) SEQ ID NO 16 (1) SEQ ID NO 17 (1) Consensus (820)									
(911) 911	920	930	940	950	096	970	086	066	1001
SEQ ID NO 2 (1)									
(1002) 1002	1010	1020	1030	1040	1050	1060	1070	1080	Section 12 1092
SEQ ID NO 11(1002) CITITCGAACACTAACCITCATITCT SEQ ID NO 2 (1)	GAACACTAACC	TTCATTTCT	ACCAGGCAGT	ACCAGGCAGTGGGGCCCCCAAGTGCAGGGCCATAGGAAGTACAAGTCTGGGAGATACTAGGCTGCAC 	STGCAGGGCC/	ATAGGAAGTA	CAAGTCTGGG	AGATACTAG(CTGCAC
SEQ ID NO 16 (1) SEQ ID NO 17 (1) Consensus(1002)									

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align SEQID#2 against SEQID#11.apr

(1093)	093	1100	5	1120	1130	1140	1150	1160	1170	Section 13
SEQ ID NO 11(1093) TGTCTGTAGAGAATCTGAAAAATA. SEQ ID NO 13 (306)	[GTCT(GTAGAGAATC	TGAAAAAATA	ATAGAGICA(ATAGAGTCACTGAAATGCAGTTTGGTATAATTATTGCCATGCATCATAATTCTAAATCATACTAGT	TTTGGTATAA5	TATIGCCAI	3CATCATAAT	TCTAAATCA1	ACTAGE
(1184) 1184 1190	184	1190	1200	1210	1220	1230	1240	1250	1260	1274
SEQ ID NO 11(1184) GGTCAAATACTCTTCCCTGAAAAAA SEQ ID NO 2 (1)	9.GTCA.	AATACICITC	CCTGAAAAAA	O D D D D D D D D D D D D D D D D D D D	TCTTGGTTTGAATTCTAAATAATTGTTGTGGTCACCACTGAGCTTTTAAATATATAAAATAC	TAAATAATTG:	TGTGGTCAC	CACTGAGCT CACTGA	TTAAATATATATATATATATATATATATATATATATAT	AAATAC
1275) 1275 1280	275 1	1280	1290	1300	1310	1320	1930	1340	1350	Section 15
SEQ ID NO 11(1275) ITICAAGITITGCATATITITATIACCTGTTCCTTAACAAACATIGAATTCAACATGAAATGATTATGGGAAACATTCGGGTATACAGTCC SEQ ID NO 13 (306)	TT	AGITIGCATA	TTTTATTAC	CIGITCOLLL	AACAAACAIIG.	AATTCAACATC	SAAAATGATT	ATGGGAAACA	ATTCGGGTATA	CAGTCC

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(13	66) 1366	1380	1390	1400	1410	1420	1430	1440	— Section 16
SEQ ID NO 11(1366) CTGACTC SEQ ID NO 2 (1) SEQ ID NO 13 (306) SEQ ID NO 15 (1)	SEQ ID NO 11(1366) CTGACTCTTAAGGACTCAGGTAAATZ SEQ ID NO 2 (1)	AAGGACTCAGGT	AAATACTTA 	GGGTATITCA	TGGCCCTAGT	CTITGGGGTA	CCACATGTTT	ACTTAGGGTATTTCATGGCCCTAGTCTTTGGGGTACCACATGTTTCTTCTTCAAATCACAGATTCA	CAGATICA
SEQ ID NO 17 (1) Consensus(1366)	(1) (1)								Section 17
(14 SEO ID NO 11(14	(1457) 1457	1470	1480	1490	1500	1510	1520	(1457) 1457 (1457) 1457 (1457) 1457 (1458) 1500 1500 1510 1520 1530 1547 (14457) 1457 (14452) 14530 1530 1530 1530 1530	1547
SEQ ID NO 2 SEQ ID NO 13 (3 SEQ ID NO 15	SEQ ID NO 2 (1)								
SEQ ID NO 16 (1) SEQ ID NO 17 (1) Consensus(1457)	(1) (1)								Section 18
(15	48) 1548	1560	1570	1580	1590	1600	1610	1620	1638
SEQ ID NO 11(1548) TTACTTG SEQ ID NO 2 (1)	.48) TTACTTGTGC (1)	CTTAAAATTTTG 	AATAGTAAA	ACAGAGIGIC	AACTICAIGC	TGGAATATTT	TIGGCTITII	SEQ ID NO 11(1548) TTACTTGTGCTTAAAATTTTGAATAGTAAAACAGAGTGTCAACTTCATGCTGGAATATTTTTGGCTTTTTAGACACAATTTTAAGTACATG SEQ ID NO 2 (1)	AGTACATG
SEQ ID NO 13 (306) SEQ ID NO 15 (1)	(1)								
SEQ ID NO 16 (1)	(1)		 						
Consensus(1548)	(1) i48)	 	 	 	 	 	 	 	

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align SEQID#2 against SEQID#11.apr

Section 19 1729 36AATCA	1820	SAT CCAC	1911	1.GGAAAC
CT AAA GAGC	1810	TAACAAATG	1900	AGCATGTAP
1710 GITATAAAA(1800	GGAAGGAAGGAAGT.	1890	CTGGGGTCAC
1700 ACIGGIAIII 	1790	GAATAGAGGA	1880	B
1690 CCITITIAAA.	1780	TTACAGGATTATTACTGAAAAAGAAATGTACGGAATAGAGGAGGAGGAGTTAACAAATGATCCAC	1870	AACAGAGCTG
1680 CAGCITICIT	1770	ACTGAAAAAC	1860	AGTGCCTAAC
1670 ACTGAAATTA 	1760	CAGGATTATT	1850	GCTTCCAGGA
1660 AAGTAACATC	1750	CTGATTATTA 	1840	CAATAAGCCT
1650 TTACAAGACT	1740	ATAATTATTA(1830	TTGAAAACACAC
(1639) 1639 (1639) AAGTATTT (1) (306) (1) (1) (1639)	(1730) 1730)) AGAAAAGC))))))))))	(1821) 1821	21) TCTGGGTGT (1) (1) (1) (1)
Section 19 1639 1639 1650 1650 1670 1680 1690 1710 1729 1	(1730	SEQ ID NO 11(1730) AGAAAAGCATAATTATTACTGATTA SEQ ID NO 2 (1)	(1821	SEQ ID NO 11(1821) TCTGGGTGTTGAAACACCCAATAAGCCTGCTTCCAGGAAGTGCCTAAGACCAGAGCTGGCTTGCTGGGTCACAGCATGTAAGGAAAC SEQ ID NO 13 (306)

align SEQID#2 against SEQID#11.apr

Section 22	FATAGCTGACA	2093	TTATGTGAATTAGCCACTATTA TTATGTGAATTAGCCACTATTA TTATGTGAATTACCACTATTA TTATGTGAATTACCACTATTA TTATGTGAATTACCACCTATTA TTATGTGAATTACCACCTATTA TTATGTGAATTACCACCTATTA TTATGTGAATTACCCACCTATTA TTATGTGAATTACCCACCTATTA TTATGTGAATTACCCACCTATTA TTATGTGAATTACCCACTATTA TTATGTGAATTACCCACTATTA TTATGTGAATTACCCACTATTA TTATGTGAATTACCCACTATTA TTATGTGAATTACCCACTATTAC TTATGTGAATTACCCACTATTAC TTATGTGAATTACCTATTACACTACAC	2184	TAACTCAGGC
1990	TAATTATGA1	2080	AAATATGTAT	2170	CCTAGGCTAT
1980	AATAATCTT	2070	AAATAACCC	2160	GCTAGICAC
1970	CCATGGGGA	2060	ATTITICAT	2150	GTTAAGACT
1960	ICCCATAGCC	2050	IGTCAAATTI	2140	CTAACCCAA
1950	GATAGATAA	2040	ATTAACTIT	2130	GITIAAAIA GITIAAAIA GITIAAAIA
1940	CAGTIGICCA	2030	CTTTATGTGA	2120	AGCTCCTAAA
1930	CACCATCCTC	2020	TGCTAAGTC	2110	GGAGAAACTGA
1920	GGCTACATGC	2010	CAAAGCACTAT	2100	CCTTAAAGA(
(1912) 1912	SEQ ID NO 11 (1912) TGCTGGGCTACATGCCACCATCCTCAGTTGTCCAGATAGAT	(2003) 2003	SEQ ID NO 11(2003) CCATTCAAAGCACTATGCTAAGTCCT SEQ ID NO 2 (1)	(2094) 2094	SEQ ID NO 11(2094) TCCTACCTTAAAGAGGAGAAACTGAGCTCCTAAAGTTTTAAATATCTTAACCCCAAGTTAAGACTGCTAGGCTATTAACTCCAGGC SEQ ID NO 2 (1)

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Section 25 2260 2275	ACTAAAAAGC	2350 2366	TICATAAAAGGAGAAAATACTGGGGAAAAGTGATAATGCAGAGTTTAAAATTTTTTGTA	2440 2457	3AGGGAGGTCTG
2250	ATAACGTCATGCT	2340	GTGATAATGCAGA	2430	AAGAAGGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
2240	TGCCTGAATT	2330	CTGGGGAAAA	2420	AAAAAAAAGG
2230	3CTTTGACTA	2320	AGAGAAATA	2410	AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
2220	CTGTTTGCAC	2310	CATAAAAGG	2400	ACCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
		2300	A	2390	
2200	GGTATAATAA	2290	TGAGCCATAG	2380	GATTGAGTAT
(2185) 2185 2190	SEQ ID NO 11(2185) AGTCTAACTCAGGTATAATAACATTA SEQ ID NO 2 (1)	(2276) 2276	SEQ ID NO 11(2276) GGGAAATAAAATGAGCCATAGGGCTC SEQ ID NO 2 (1)	(2367) 2367	SEQ ID NO 11(2367) AAAGTGCCAGAGATTGAGTATAACAA SEQ ID NO 2 (1)

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(24	(2458) 2458	2470	2480	2490	2500	2510	2520	2530	Section 282548
SEQ ID NO 11(2458) AAT SEQ ID NO 2 (1) SEQ ID NO 13 (306) SEQ ID NO 15 (1) SEQ ID NO 16 (1) SEQ ID NO 17 (1) Consensus(2458)	58) AATAGAAAT (1) 06) (1) (1) (1) (1)	SEQ ID NO 11(2458) AATAGAAATATCAGAGGAAGGAAATZ SEQ ID NO 2 (1)ATCAGAGGAAGGAAATZ SEQ ID NO 13 (306)	GGAAATAAAC GGAAATAAAC 	3GAGGGTGAGA	GTAAATICTC	TTTTAGCATT TTTTAGCATT TTTTAGCATT	CAGATTCCAC. CAGATTCCAC.	SEQ ID NO 11(2458) AATAGAAATATCCACAGAAGGAAGTGAGGGTGAGGTGAAATTCTCTTTTAGCATTCCACAGATTCCACACAATCCACATTTCT SEQ ID NO 2 (1)ATCAGAGGAAGTAAAGGAGGGTGAGGTAAATTCTCTTTTTAGCATTCCACAGATTCCACACAATCCTACTTTTT SEQ ID NO 13 (306)	CATITICT CATITICT
(30)	(25.40) 25.40	25.80	0570	2580	2500	0800	0830	2620	Section 29
SEQ ID NO 11(2549) TIT SEQ ID NO 2 (83) TIT SEQ ID NO 13 (306) SEQ ID NO 15 (1)	49) TITITACC 33) TITITACC 36) (1)	SEQ ID NO 11(2549) TITITIACCAACTAAGGAAAATAACACTIGACCTAACATTICATIGCAGITAGCTAAAGGAIGCTAGAAAAACTAIGT SEQ ID NO 2 (83) TITITIACCAACTAAGGAAAAATAACACTIGACCTAACATTICATIGCAGTIAGCTAAAGGAIGCTAGAAAACTAIGT SEQ ID NO 13 (306)	AAATAACAC1 AAATAACAC1 	TIGACCIAACA TIGACCIAACA	TTTCATTGCF	GTTAGCTAAA	GGATGCTAGA GGATGCTAGA 	SEQ ID NO 11(2549) TITITACCAACTAAGGAAAATAACACTTGACCTAACATTTCATTGCAGTTAGGTAAAGGATGCTAGAAAACTATGTTGCAGTGGTTTG SEQ ID NO 13 (306)	TGCAGTGGTTTG TGCAGTGGTTTG
SEQ ID NO 16 (1) SEQ ID NO 17 (1) Consensus(2549)	(1) (1)								Section 30
(26	(2640) 2640	2650	2660	2670	2680	2690	2700	2710 2720	2730
SEQ ID NO 11(2640) CTCT SEQ ID NO 2 (174) CTCT SEQ ID NO 13 (306)	40) CTCTAATT1 74) CTCTAATT1 16)	ICTTCAGGAAT! ICTTCAGGAAT!	AGAGAAAAG1 AGAGAAAAG1 	IGACAAAAAGA IGACAAAAAAA 	TCAGAGAAGP .TCAGAGAAGP	1GAAGAAAGGA 1GAAGAAAGGA 	AACTATCAGAA AACTATCAGAA 	SEQ ID NO 11(2640) CTCTAATTTCTTCAGGAATAGAGAAAGTGACAAAAGATCAGAGAAGAAAGA	SAGTAGGA SAGTAGGA
SEQ ID NO 15 SEQ ID NO 16	(1)								
SEQ ID NO 17 (1) Consensus(2640)	(1) 40)								

align SEQID#2 against SEQID#11.apr

2740 ATATIT ATATIT
Section 31 2731 2740 2750 2760 2770 2780 2790 2800 2821 2

SECION 01 (13004) 3004 3010 3020 3030 3040 305
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			GIGIIGGIAA			 &&&&TITI &AAAATITI	SEQ ID NO 15 (1)	(1) (1) (09) TEATICIAC (59) TIATICIAC
TITAAATITCAACTGITGGGGGGGTGGTAATGTAAAACAAACTCAGTAGTAGTATTCAGTA TITAAAITTCAACTGTIGGGCGTGTIGGTAATGTAAAACAAACTCAGTAGTAGTATTCAGTA 	ACTCAGTACAG1 ACTCAGTACAG1 	rgtaaaacaai rgtaaaacaai 	GIGIIGGIAA GIGIIGGIAA	:GTTGCGCGT :GTTGCGCGT	AATTTCAAC AATTTCAAC 		SEQ ID NO 11(3459) TTATTCTACGTTTTTGTCCAAAAAT SEQ ID NO 2 (993) TTATTCTACGTTTTTGTCCAAAAAT SEQ ID NO 13 (306)	SEQ ID NO 11(3459) TTATTCTA SEQ ID NO 2 (993) TTATTCTA SEQ ID NO 13 (306)
Section 39 3549	3530	3520	3510	3500	3490	1	3470	(3459) 3459
			 AGCCAGGTAT AGCCAGGTAT	 ACTICATAA ACTITCATAA		 GATGTGTGAG GATGTGTGAG	SEQ ID NO 16 (1)SEQ ID NO 17 (218) TATICICCIACCCIGAGITGAIGIG Consensus(3368) TATICICCIACCCIGAGITGAIGIG	(1) 18) TATICICC 68) TATICICC
3450 3440 3440 3450 3450 3450 3450 3450	344U TAGGTAAGTAAJ				 			SEQ ID NO 13 (306) SEQ ID NO 15 (1)
TTACATTTCTA Section 38		3450 3440 3450 3450 3450 3450 3450 3440 3450 345	3420 AGCCAGGTAT AGCCAGGTAT	3410 ACTITCATAA ACTITCATAA	3400 CAATAIGIO	3390 3A TG TG TG AG 3A TG TG TG AG	3380 ACCCTGAG 	3368 TATTCTC TATTCTC)
TIACATITGIA	[AAGATATTAT]	AATIACIICI 3430 ACATTAIGGAA	3420 3420 AGCCAGGTAT AGCCAGGTAT	3410 3410 ACTITCATAA.	3400 CANTAIGICA	3390 3390 3A1G1G1GAG 3A1G1G1GAG	3380 TACCCTGAGTT TACCCTGAGTT 	(326) GAAATAAA (3368) 3368 (3368) TATTCTCC (902) TATTCTCC (306)
		AATTACTICT AATTACTICT AATTACTICT 3430 ACATTATGGA(ACATTATGGA(ACATTATGGA(ACATATATATGGA(ACATATATGGA(ACATATATATGGA(ACATATATGGA(ACATATATGGA(ACATATATATGGA(ACATATATGGA(ACATATATGGA(ACATATATGGA(ACATATATGGA(ACATATATATGGA(ACATATATATGGA(ACATATATATGGA(ACATATATATGGA(ACATATATATGGA(ACATATATATGGA(ACATATATATGGA(ACATATATATGGA(ACATATATATATGGA(ACATATATATATGGA(ACATATATATATGGA(ACATATATATATGGA(ACATATATATATGGA(ACATATATATATGGA(ACATATATATATGGA(ACATATATATATATATATGGA(ACATATATATATATATATGGA(ACATATATATATATATATATATATATATATATATATAT		3410 ACTTCATAA	TICICAAAA(TICICAAAA(TICICAAAA(CAATATGICAAAA(CAATATGICAAAAA(CAATATGICAAAAA(CAATATGICAAAAA(CAATATGICAAAAA(CAATATGICAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	ATTATTIATT TTATTIATT 3390 SATGTGTGAG	SEQ ID NO 15 (1)	(1) 27) GAAATAAA 77) GAAATAAA 68) 3368 68) TATTCTCC 02) TATTCTCC 06)
TATTTTCTCAAAACAACAATACGATTTAGCAAATTACTTCTTAAGATATTTTTTACATTTCTA TATTTTCTCAAAACAACAACAATTTAGCAAATTACTTCTTAAGATATTTTTTACATTTCTA TATTTTCTCAAAACAACAACAAGAATACGATTTAGCAAATTACTTAAGATATTATTTTTCTA TATTTTCTCAAAACAACAACAAATACGATTTTCTA	TAAGATATTATT TAAGATATTATT	AATTACTTCT AATTACTTCT AATTACTTCT AATTACTTCT AATTACTTCT AATTACTTCT AATTACTTCT AATTACTTCT ACATTATGGA ACATTATGGA	CGATTTAGCA CGATTTAGCA CGATTTAGCA CGATTTAGCA CGATTTAGCA CGATTTAGCA CGATTTAGCA CGATTTAGCA CGATTTAGCA AGCCAGGTAT	AACAGAATA	TTCTCAAAAAATCTCTCAAAAAAAAAAAAAAAAAAAAA	######################################	SEQ ID NO 11(3277) GAASTAAATAAGCTGATTATITATT SEQ ID NO 2 (811) GAAATAAATAAGCTGATTATITATT SEQ ID NO 13 (306)	SEQ ID NO 11(3277) GAAATAAAT SEQ ID NO 2 (811) GAAATAAAT SEQ ID NO 13 (306) SEQ ID NO 15 (1) SEQ ID NO 16 (1) SEQ ID NO 17 (127) GAAATAAAT Consensus(3277) GAAATAAAT (3368) 3368 SEQ ID NO 11(3368) TATTCTCCT SEQ ID NO 2 (902) TATTCTCCT SEQ ID NO 13 (306)

align SEQID#2 against SEQID#11.apr

(3550) 3550	3560	1	3580	3590	3600	3610	3620	3630	3640
SEQ ID NO 11(3550) CAGTAT SEQ ID NO 2(1084) CAGTAT SEQ ID NO 13 (306) SEO ID NO 15 (1)	SEQ ID NO 11(3550) CAGTATTTAAGCCCCTGTACTTAAAC SEQ ID NO 2(1084) CAGTATTTAAGCCCCTGTACTTAAAC SEQ ID NO 13 (306)SEQ ID NO 15 (1)SEQ ID NO 15 (1)	$\alpha \alpha $	TATICCICGI. TATICCICGI.	ACCAATGAAG ACCAATGAAG 	TTACATGAAA TTACATGAAA 	AGCAAAIIIC AGCAAAIIIC 	TATICCICGTACCAAIGAAGITACAIGAAAAGCAAAITIGIGIGAGAIAICGIAGAIGGAAGIA TAIICCICGIACCAAIGAAGIIACAIGAAAAGCAAAIIIGIGIGAGAIAICGIAGAIGGAAGIA 	CGTAGATGG CGTAGATGG	AAGTA AAGTA
SEQ ID NO 17 (367) SEQ ID NO 17 (367) Consensus(3550)									
(3641) 3641	3650	3660	3670	3680	3690	3700	3710	3720	3731
SEQ ID NO 11(3641) AATTAC SEQ ID NO 2(1175) AATTAC SEQ ID NO 13 (306) SEQ ID NO 15 (1) SEQ ID NO 16 (1) SEQ ID NO 16 (1) SEQ ID NO 17 (367)	SEQ ID NO 11(3641) AATTAGTCTTTATGTTCCCCACAAAT SEQ ID NO 2(1175) AATTAGTCTTTATGTTCCCCACAAAT SEQ ID NO 13 (306)	\vdash	TGAAATGCATTTCAAAAACTCTGTGTGT TGAAATGCATTTCAAAAACTCTGTGTGTGT	TCAAAAACTC TCAAAAACTC	TGTGTGTGTA	TGTGTGTGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	GAAATGCATTTCAAAAACTCTGTGTGTGTGTGTGTGTGTG	IGTGTGAGA	GAGAG GAGAG
		0		To Sender O	i i				Section 42
(3732) 3732 (3732) ACAGAG (1266) ACAGAG	SEQ ID NO 11(3732) 3732 3740 3750 SEQ ID NO 11(3732) ACAGAGAGATACGCTTTGGTTGCCTC SEQ ID NO 2(1266) ACAGAGAGATACGCTTTGGTTGCCTC		3760 ATAAGCIGGC ATAAGCIGGC	3770 TGCTATGATT TGCTATGATT	3780 AATAAGACCA AATAAGACCA	3790 AGTTTTCTA/ AGTTTTCTA/	3760 3770 3780 3780 3802 3800 3810 3822 CATAAGCTGGCTGCTATGATTAATAAGACCAAGTTTTCTAAAGAAAATGAGATCATAACAAAAGC CATAAGCTGGCTGCTATGATTAATAAGACCAAGTTTTCTAAAGAAAATGAGATCATAACAAAAGC	3810 ATCATAACA ATCATAACA	3822 AAAGC AAAGC
SEQ ID NO 13 (308) SEQ ID NO 15 (1) SEO ID NO 16 (1)									
SEQ ID NO 17 (367)									
Consensus(3732)									

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3913	TICACAA ITCACAA 	TICACAA	TTCACAA Section 44	4004	4 E O C C C C C C C C C C C C C C C C C C		GCCTCTA Section 45	4095	TAAATAT	TARAIAI 	
3900	ATGAAAATTCA STGAAAATTCA 	GGGCAAAAGGAAAAGAGACAAAACAGCATGAAATGATGAGACCAAGTGAAAATTCATTC	GGGCAAAAAGGAAAGACAAAACAGCATGAAATGATGAGACCAAGTGATGAAAATTCACAAAAAA Section 44	3990	TIGGGTAATICAGCAGCCIGITACTATGGCTCICIGGAGIGATAGCTAATGTAATG	CIGGAGIGAIASCIAAIGIAAAIGAAGCOICIA	CTGGAGTGATAGCTAATGTAAATGAAGCCTCTA CTGGAGTGATAGCTAATGTAAATGAAGCCTCTA Section 45	4080	TACTCAGCCAATAATGCAACAGAAATGCATTCAAAGCATTGGGGAAAAATTCAAAAGAATAATAT TACTCAGCCAATAATGCAACAGAAATCCATTGAAAGCATTGGGGAAAAATTCAAAAGAATATA	TACICAGCCAATAATGCAAAAGCATTCCATTCAAAGCATTCGGGAAAAATTCAAAGAATAATAAT	
3890	GACCAAGIGA GACCAAGIGA 	GACCAAGIGA	GACCAAGIGA	3980	TGATAGGTA?	TSATASCTA?	TGATAGCTAP	4070	TCGGGAAAAA	TCGGGAAAA	
3880	GAAATGATGA GAAATGATGA 	GARAIGATGA	 GAAATGATGA	3970	CTCTCTGGAC	CICICIGGAC	CICICIGGAG	4060	TTCAAAGCAT TTCAAAGCA1	TTCAAAGCA1	
3870	AAAACAGCAT AAAACAGCAT 	RARACAGORI 	 AAAACAGCAT	3960	GITACIAIGG	GTTACTATEG	GITACIAIGG	4050	CAGAAAICCA CAGAAAICCA	CAGAAATCCA 	
3860	GGAAAGAGAC GGAAAGAGAC 	GGAAAGAGAC	GGAAAGAGAC	3950	TCAGCAGCCT	TGGGTAATICAGCAGCCTGTTACTATSGCTCT	TGGGTAATICAGCAGCCTGTTACTATGGCTCT	4040	AATAATGCAA AATAATGCAA	 ^AATAATGCAA 	
3850	GGGGCAAAAA GGGGCAAAA 	-6666AAAAA	GGGCAAAAA	3940	CIIGGGIAAI CIIGGGIAAI	14-4	[4030	ATACTCAGCC ATACTCAGCC	ATACICAGCC 	
3840	ICTTTTATCA ICTTTTATCA 			3930	AGTAATTICI AGTAATTICI	GAGTAATTICI		4020	IGACAAGAAT IGACAAGAAT	rgacaagaat 	
3830	TTATGACTA: TTATGACTA:			3920	GCITICAAG	GCTITCAAGA		4010	GGATTAICC	GGATIAICC	
(3823) 3823	SEQ ID NO 11(3823) CCTCTTTATGACTATCTTTTATCAGGGGCAAAAGGAAAGACAAAACAGCATGAAATGATGAGGACCAAGTGAAAATTCATTC	SEQ ID NO 15 (1)	SEQ ID NO 17 (367) Consensus(3823)	(3914) 3914	SEQ ID NO 11(3914) TGATTGCTTTCAAGAGTAATTTCTC SEQ ID NO 2(1448) TGATTGCTTTCAAGAGTAATTTCTC SEO ID NO 13 (206)	SEQ ID NO 15 (67) IGATISCITICAAGAGIAAITICIC SEQ ID NO 16 (1)	SEQ ID NO 17 (367)	(4005) 4005 4010	SEQ ID NO 11(4005) AAAGTGGATTATCCTGACAAGAATATACTCAGCCAATAATGCAAGAAATGCATTCAAAGCATTCGGGAAAAATTCAAAGAATAAATA	SEQ ID NO 15 (158) AAAGTGSATIATCCTGACAAGAATA SEQ ID NO 16 (1)	SEO ID NO 17 (367)
	SEQ ID NC SEQ ID N SEQ ID NC	SEQ ID NC	SEQ ID NC Consen		SEQ ID NC SEQ ID N	SEQ ID NO 15 SEQ ID NO 16	SEQ ID NC Consen		SEQ ID NC SEQ ID N	SEQ ID NC SEQ ID NC	OFO ID NO

SEQ ID NO 11(4096) TOTTTTTTTTTAAAGITAATG	TITITIAAAGI	4120 TAAIGACCIA	ACCTACGATCCATT	4140 CTICCCIGAC	4150 TAACAAGCAC	4160 SCAAGCACFI	4140 4150 4160 4170 4186 CITCCTGACTAAAATATCCAGCCAGGATGAA	4186 CAGGATGAA
SEQ ID NO 2(1630) TCTTTTTTTTTTAAAGTTAATGACCTACGATCCATTTCTTCCCTGACTAACAAGCAGCAGCACTTAAAAATATCCAGGATGAA SEQ ID NO 5 (1630) TCTTTTTTTTTTTTTTTCCAGGATGAA SEQ ID NO 13 (306)	ITTTTAAAGT 	TAATGACCTA 	CGATCCAITI 	OTTCCCTGAC 	TAACAAGCAC 	SCAAGCACTT 	ACCTACGATCCATTTCTTCCCTGACTAACAAGCAGCAAGCA	CAGGATGAA
	 TTTTTTAAAGT 4200	TAATGACCTA	 CGATCCATTT 4220	 CITCCCTGAC 4230	TAACAAGCAC	 GCAAGCACII 4250		CAGGATGAA Section 47
SEQ ID NO 11(4187) ATAGAAACCCACCTGACTTGTTAATATTTTTGTTTGGTCCCAGGGACTCAGATTCTAAGCCAAATTCTTTGAATGATCTTGGCAAATGTCT SEQ ID NO 2(1721) ATAGAAACCCACCTGACTTGTTAATATTTTTGTTTGGTCCCAGGGACTCAGATTCTAAGCCAAATTCTTTGAATGATCTTGGCAAATGTCT SEC ID NO 13 (2002)	SACCTGACTTG	TIAAIATITT Ilaaiaitit	ATTITIGITISGICCCASSACTCASATICTAASCCAAAITCII ATITIGITISGICCCASSGACTCASATICIAAGCCAAAITCII	CAGGGACTCA	GATICTAAG	CAAATICTI	TGAATGATCTTGGCAAATGTCT	CAAATGICI
SEQ ID NO 15 (340) AIASAACCAACCIGACIIGIIAAI SEQ ID NO 16 (1)	3ACCTGACTTG	 	TGTTTGGTC	CAGGGACICA	SATICIAAG	CARAIICI	TITGITISGICCCAGGGACTCASALICIAAGCCAAAITCITIGAATGATCTISGCAAA	
SEQ ID NO 17 (367) Consensus(4187) ATAGAAACCCACCTGACTTGTTAAT	CACCTGACTTG	TTAATATTT	TGTTTGGTCC	CAGGGACICA	 .GATTCTAAG(CAAATICII	TGTTTGGTCCCAGGGACTCAGATTCTAAGCCAAATTCTTTGAATGATCTTGGCAAATGTCT Section 48	CAAATGTCT Section 48
(4278) 4278	4290	4300	4310	4320	4330	4340	4350	4368
SEQ ID NO 11(4278) CGAATTATTTTTGCCAACTTTTCTT SEQ ID NO 2(1812) CGAATTATTTTTGCCAACTTTTCTT SEO ID NO 13 (206)	TITGCCAACTI	TICTITATOL	TATCTTGGAAAAAAGTTTCATGAATGGGTGTCAAAATTGATT TATCTTGGAAAAAAGTTTCATGAATGGGTGTCAAAATTGATT	GITICAIGAA GITICAIGAA	TGGGTGTCA/	AATTGATTA AAATTGATTA	GITIA	ITCTIGCAG
SEG ID NO 13 (300)	TTGCCAACIT	5-4	TGGAAAAAA	GTTTCATGAA	TGGGTGTCAA	 Leatea	ATCTIGGAAAAAAGITICAIGAAIGGGIGICAAAAITGAFIAGIITIAAAAACCIITCT	TICTIGCAG
SEQ ID NO 18 (1)	F						\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\	

align SEQID#2 against SEQID#11.apr

(4369) 4369	4369	4380	4390	4400	4410	4420	4430	4440		Section 49 4459
SEQ ID NO 11(4369) ATACGTATGGCACCCTAAAACTGTATTAGAAAAAGTAAGT	ATACGTA ATACGTA	TGGCACCUR	AAACTGTATTA AAACTGTATTA	TTAGAAAAAAAGT TTAGAAAAAAA 	FAAGTACTCT	GTAGTGTGA; 	AAAATTCTTA <i>?</i> 	AAGGACACCC7	CTTTTACA	AACTCA
SEQ ID NO 15 (522) ATACSTATSGCACCCTAAAACTGTAT SEQ ID NO 16 (1)	ATACGIA 	TEGCACCCTA	ABACTGTATI?	TAGAAAAAA. 						
SEQ ID NO 17 (367)		IGGCACCCIA								
(4460) 4460	1460	4470	4480	4490	4500	4510	4520	4530	4540	4550
SEQ ID NO 13 (306)										Section 51
(4551) 4551	1551	4560	4570	4580	4590	4600	4610	4620	4630	4641
SEQ ID NO 11(4551) TGGCAGGTGTGGTGGTTCCACCTGTAATTCCAGCACTTTGGGAGGCCGAGGCGGGCG	TGGCAGG	TGTGGTGGCT	CACACCIGIAF	ATTCCAGCACT	LTTGGGAGGC	CAAGGCGGG(GGATCACCTG	3AGATCAGGA(TTCAGGAC	CAGCC
SEQ ID NO 16 (1) SEQ ID NO 17 (367) Consensus(4551)										

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align SEQID#2 against SEQID#11.apr

4720 4732	TACTGAAATACAAAAATCACCCGGGTGTGGGTGACGGCCCTGTAGTCCCAGCTACTCGGGTAGC	4810 4823	3 G G T G A C A G A G C A A G A G A G A G A G A	4900 4914	CCCAGTCAATTGTTTT
4710	SCCIGIAGICCC	4800	CACTCCAGCCTC	4890	3GAAATATTCAC
4700	GGTGACGGGCC	4790	CATGCCACTGC	4880	CCCTCTGCAT(
4690	CACCCGGGIG1	4780	T G A G C T G A G A T A C A G C T G A G A T A C A C T A C A C A C A C A C A C A	4870	GCTATICCCAC
4680	ATACAAAAAT	4770	GAGGTTGCAG	4860	TTTTTCAACA
4670	TTTACTGAAA	4760	TCAGGAGTCA	4850	AAAAGACTGG
4660	5AAACCCAGTC	4750	ATCACTTGAAC	4840	AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
4650	CAATATGGTC	4740	3 G C A G G A G A A	4830	CATCTCAAAA
(4642) 4642	SEQ ID NO 11(4642) GATCAATATGGTGAAACCCCAGTCTT SEQ ID NO 2(1939)	(4733) 4733	SEQ ID NO 21(4733) TGAGGCAGGAGAATCACTTGAACTCAGGAGTTGCAGTGAGCTGAGATCATGCCACTGCACTCCAGCCTGGGTGACAAGA SEQ ID NO 2(1939)	(4824) 4824	SEQ ID NO 11(4824) CTCCATCTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

align SEQID#2 against SEQID#11.apr

(4915) 4915 4920	4920	4930	4940	4950	4960	4970	4980	4990	5005
SEQ ID NO 2(1939)	STITGGGTA	ATGGCCCTC	TGGGCAGGA(CTGGAGTGGG	GCACACAGGA 	GAAGCTGCAF	ACTATGTTT.	AGAAGCAIGICIG	3GAAATGT
(2006) 5006		5020	5030	5040	5050	5060	5070	5080	5096
SEQ ID NO 17 (367) Consensus(5006)									
(2097) 5097		5110	5120	5130	5140	5150	5160	5170	5187
SEQ ID NO 11(5097) GAGAAGCAAAAGTGGGGAAGCAAGAAGTAATGCTTTTCATCAGCCAAAT SEQ ID NO 2(1939)	AGCAAAAGT	GGGGAAGCA	AGAGGAATT/	ATGCTTTTCA	TCAGCCAAAT	TTGCAGGTAG	GAGGATIGG	TIGCAGGTAGGAGGATTGGCTCAGTCATCTTGGCTGAGGC	3CTGAGGC

align SEQID#2 against SEQID#11.apr

(5188) 5188	5200	5210	5220	5230	5240	5250	5260	5278
SEQ ID NO 11(5188) TCATGAAACCAGGTGTAAAGAAAGTGGACTAGATTACATCATTACAGGAAGAAGAAGATAATCCAGGAAGAAACCATTGGGA SEQ ID NO 2(1939)	ACCAGGTGTAA	AGAAAGIGGA	CTAGATTAAT:	FTCATCCATI	ACAGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA	GAGCCGTGAA	AGATAATCCAG;	AAATCATTGGG
(5279) 5279	5290	5300	5310	5320	5330	5340	5350	Section 59 5369
SEQ ID NO 2(1939)		C			H	-		20
(5370) 5370	5380	5390	5400	5410	5420	5430	5440	5450 5460
SEQ ID NO 11(5370) TACCCATGAGTTGACTCAGAAAAA SEQ ID NO 2(1939)	GAGITGACICA(GAAAAACAT	AAAAGTATT(STIGCICIGC	TCAGAGITIT	ATCTAACTCA	CATAAAAAGIATIGITGCTCIGCICAGAGITITIAICIAACICAIICICACITCITAITCCAIGAIG	IATICCAIGAI
SEQ ID NO 16 (1)								
SEQ ID NO 17 (367)								
Consensus(5370)								

align SEQID#2 against SEQID#11.apr

(5461) 5461	5470	5480	5490	5500	5510	5520	5530	5540	5551 5551
SEQ ID NO 11(5461) AAATGASEQ ID NO 2(1939) SEQ ID NO 13 (306) SEQ ID NO 15 (558) SEQ ID NO 16 (1) SEQ ID NO 17 (367) Consensus(5461)	SEQ ID NO 11(5461) AAAIGACAIAAAIGAGGIIITIIAI SEQ ID NO 2(1939)	GGTTTTTTAT:		IGITGITGITGITTITCIGACACAAGGCAAGGIAGCIACCIGGGCAGAGCIGITITAITICIC	GGACACAAGG	CAAGGIAGC	TACCTGGGCA	GAGCTGTTTT	ATTICIC
(5552) 5552	5560	5570	5580	5590	5600	5610	5620	5630	5642
SEQ ID NO 2(1939) SEQ ID NO 13 (306) SEQ ID NO 15 (558) SEQ ID NO 16 (1) SEQ ID NO 17 (367) Consensus(5552)									
(5643) 5643	5650	5680	5670	5680	5690	5700	5710	5720	5733
SEQ ID NO 11(5643) GCATCCTT SEQ ID NO 2(1939) SEQ ID NO 13 (306) SEQ ID NO 15 (558) SEQ ID NO 16 (1) SEQ ID NO 17 (367)	CTTCCCTGTCCTTCCTTCTTCTCTTCTTCTTCTTCTTCTT		ATTGTTGGTG	TIGITGGTGATGACAATGTCTCTCCCATCAGCCTCATGAAGTTCTCTCTC	CTCCCATC	AGCCTCATG,	AAGTICTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTC	TCATITATIA	AAATTTG
Consensus (5643)									

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align SEQID#2 against SEQID#11.apr

(5734) 5734 5740	5740	5750	5760	5770	5780	5790	5800	5810	Section 64 5824
SEQ ID NO 11(5734) CTTTCAGGAAAAATTTTGAAAATGT SEQ ID NO 2(1939)	XAGGAAAAAT	TTTGAAAATC	STGTCCAGTA/	ATGCCTGATT	SGCCCTTATC	CTAAAGGCTC	AAACTGGAG	GTCCAGTAATGCCTGATTGGCCCCTTATCCTAAAGGCTTAAACTGGAGGAAGGA	AACTGAG
(5825) 5825 5830	5830	5840	5850	5860	5870	5880	5890	5900	5915
SEQ ID NO 11(5825) AAATCTTGCAAATCATTGAGCCAAAAACGTAT SEQ ID NO 2(1939)	TTGCAAATC	SATTGAGCCAA	AAAACGTATTA	TAATAGCAAGATCTATCAT	CTATCATTT/	TTATIGACTAGIAIGIGGCAGGCAGIGCCCT	ATGTGGCAGG	\vdash \vdash \vdash \vdash \vdash \vdash	TTATTTAG
(5016) 5018		2030	5040	0202	5080	5070	Cada	2000	Section 66
SEQ ID NO 15 (558)	GAGAGTTGA	ATGGGGGGGG	09440 0GGGGTTCAC7	ACAICITAAA(3AGGTGCTATC	TCCTCTATA	ATAAATCATG	TAAGTCAAGAG	AGTAAGG
SEQ ID NO 17 (367) Consensus(5916)									

align SEQID#2 against SEQID#11.apr

2009 (2009)	6020	9030	6040	6050	0909	6070	6080	Section 67 6097
SEQ ID NO 11(6007) AATTGTCTTTGTTTTGTTTTATTCAGGGGATTAGAGTATACAGTAGAAGATCCCCAAGAAACCTTGGGATCATTTTAGACTAAGAAATGCCAAGAAACCCAAGAAACCCTTGGGATCATTTTAGACTAAGAAATGCCAAGAAACCCAAGAAACCCAAGAAACCCAAGAAACCCAAGAAACCCAAGAAACCCAAGAAACCCAAGAAACCCAAGAAACCCAAGAAACCCAAGAAACCCAAGAAACCCAAGAAACCCAAGAAACCCAAGAAACCCAAGAAACCCAAGAAACCCAAGAAACCCAAGAAAAACCCAAGAAAACCCAAGAAAACCCAAGAAAACCCAAGAAAACCCAAGAAAACCCAAGAAAAACCCAAGAAAACCCAAGAAAACCCAAGAAAAACCCAAGAAAAACCCAAGAAAAACCCAAGAAAAACCCAAGAAAAACCCAAAAAA	GTCTTTGTTTGGTTP	TATTCAGGGG	SATTAGAGTAT	ACAGTAGAAG	ATCCCAAGAA	ACCTTGGGAT	CATTTTAGACTAAGA	AATGCCA
8609 (8609)	6110	6120	6130	6140	6150	9160	6170	- Section 68 6188
SEQ ID NO 11(6098) ATACCGCCGGGCGCGGTCACCTCTAATCCCAGCACTTTGAGAGGCCGAGGTGGGCGGATCACAAGGTCAGGAGTTGAGACCGTC SEQ ID NO 2(1939)	CGCCGGCCGGGTGG	CTCACGCCTG	STAATCCCAGC	ACTTTGAGAG	GCCGAGGTGG	GCGGATCACA	AAGGTCAGGAGATTGA	GACCGTC
SEQ ID NO 17 (367) Consensus(6098)								
(6189) 6189 (6189) 6189	6200	6210	6220	6230	6240	6250	6260	6279
SEQ ID NO 1 (6189) CIGGCTAACGIGGIGAAACCCIGICICIACIAAAAAITAGCCGGGCGIGGIGGIGGCGCGCCIGIAGICCCAGCTACICGGGAAAAAAAAAA	CIAACGIGGIGAAAC 		ACTABABATAC 	AAAAATTAG 	9 9 1 1 1		CIGIAGICCCAGCIA	C.I.C.G.G.B.A.
SEQ ID NO 16 (1) SEQ ID NO 17 (367)								
Consensus(6189)								

align SEQID#2 against SEQID#11.apr

(6280) (6280)	9530	6300	6310	6320	6330	6340	6350	6360	Section 70 6370
SEQ ID NO 11(6280) GGCGGAGGCAGGAATGGTGTGTAA SEQ ID NO 2(1939)	GGAGGCAGGAGAAAA	ATGGTGTAAC:	ICAGGAGGCG	GAGCTTGCAG	CTCAGGAGCGGAGCTTGCAGTCAGCCGAGATTGCCCCAATGCACTCCAGCCTGGGCGACAGAACG	TGCCCCAATC	SCACTCCAGCC	TGGGCGAC	:AGAACG
(6371) 6371	6380	6390	6400	6410	6420	6430	6440	6450	6461
SEQ ID NO 11(6371) AGACTCCGTCTCAGAACAAAAASEQ ID NO 2(1939)	CTCCGTCTCAGAA	ACAAAACAAAA(3GAAATGCCA.	ATACCAGGAG	AGGAAATGCCAATACCAGCAGAAATAGAGCCAAATCATGAACATAAGCTAAACAAATGTTGGCAGT	AATCATGAAC	ATAAGCTAAAA	CAAATGTT	GGCAGT
(6462) 6462	6470	6480	6490	6500	6510	6520	6530	6540	Section 72 6552
SEQ ID NO 11(6462) GTAGCCTAGTGGTTAAGAGGAGCAGACTCTTAACTAGAACACTGCACTCCATGTCCTCACTGTAGACCCTCACTGTGGGGTTCTAATTAACC SEQ ID NO 2(1939)	GCCTAGTGGTTAAA	AAGAGAGCAGACT	ICTTAACTAG.	AACACTGCAC	TCCATC	ACTGTAGACO	CC TC T	GGTTCTAP	TTAACC
Consensus(6462)									

align SEQID#2 against SEQID#11.apr

6610 6620 6630 6643	ICATCTGTAGAAGGGGT	6710 6720	TTAAAATGCTGCTCCAAAAGAGTTTTGTTA	6800 6810 6825	SEQ ID NO 11(6735) ACTTAAGAACTGATTTACTTGCATCTAAACTGACAGGTCTACTTGGAAATGATCAAGCATGGTCTACAA SEQ ID NO 2(1939)
99 0099	TTGTGCCCCAATTT	0029 0699	GTATITGTAAAGTG	6780 6790	AACTGGAAATGATC
6590	TTCCTTAAGTTCG	0899	ATGAGITACTACI	6770	GACAGCTCTCAAT
6580	GTCTTAAGGCA	0299	GTGAGCATTAA 	6760	GCATCTAAAACT
0 6570	TACCAGIGGCA	0999	ATAGGCTTACT	6750	CIGATITACITI
(6553) 6553 6560	H	(6644) 6644 6650	SEQ ID NO 11(6644) GTTTACTTT2 SEQ ID NO 2(1939)	(6735) 6735 6740	SEQ ID NO 11 (6735) ACTTAAGAACTGA SEQ ID NO 2(1939)

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align SEQID#2 against SEQID#11.apr

(6826) 6826	6840	6850	0989	6870	6880	0689	0069	— Section 76 6916
SEQ ID NO 11 (6826) TGAAGGCAAAAATGTTCGTTTCTTT SEQ ID NO 2(1939)	\GGCAAAAATGTTCGT]	TCTTTTGTT	CAGCCCTGTGTGCCCTGTGTGCTGCTGTGCTGTGTGTGTG	CCTAGATCAA	FATCTAGTGAT	CATGCTCAA(TGTTCAGCCCTGTGCCTAGATCAATATCTAGTGATCATGCTCAAGAAATATTGTTGAATGAA	TGAATCAA
(6917) 6917	0830	6940	6950	0969	0269	6980	0669	7007
SEQ ID NO 11(6917) TGAACCTACCGAGGTAGTTACATAAAAGAGT SEQ ID NO 2(1939)	ACCTACCGAGGTAGTT7	ACATAAAAGA	GTTCTGCATG/	AGTACAAATC:	IGGGCAAAGTC	SACCICCAAGG	TCTGCATGAGTACAAATCTGGGCAAAGTGACCTCCAAGGAAATTTCCACTTT	TTTAGATTCT
(7008) 7008	7020	7030	7040	7050	7060	7070	7080	Section 78 7098
SEQ ID NO 11(7008) GTGATTTCCTTAAGGAACTGATAAAT SEQ ID NO 2(1939)	ATTCCTTAAGGAACTC	ATAAATTGG	TGTGATACAA	GTAAAAAAA 	TGGTGTGATACAATGTAAAAATGTGCCTATATGATTTGAGAAAAACTTA	GATTTGAGA/		
Consensus(7008)								

align SEQID#2 against SEQID#11.apr

990Z (990Z)	2000	7110	7400	7130	7140	7450	7480	24.70	Section 79	on 79
SEQ ID NO 11(7099) TITITCCTTCCTTCCTCCTCCTCCTCCTCCTCCTCCTCCT		THCCHICCHI		H H C C H H C C H H C C H H C C H H C C H H C C H C H C C H C C H C C H C C C H C		TTCCTTCCTC	CCTTCCTTCCTTCCTTCCTTCCTTCCTCCCTCCCTTCCTTCTTTT	TTCCTTCCTTCTTCTTTTTTTTTTTTTTTTTTTTTTTTT	TCTTTCTTCT	
(7190) 7190	7190	7200	7210	7220	7230	7240	7250	7260	7270 7280	7280
SEQ ID NO 11(7190) CITICITICITICITICITICITICITICITICITICIT	CITICII.	TCTTTCTTTC		TCTTTCTTTC	CHTICITICE	TCTTCTTT	1CTCTTTCCTTTCTTTCTTTCTTTGTGTGCCTTT	CHTTCTTCCTT	TCTTTGTGCC	
SEQ ID NO 16 (1) SEQ ID NO 17 (367) Consensus(7190)		1		1						6
(7281)	7281	7290	7300	7310	7320	7330	7340	7350	7360	7371
SEQ ID NO 11(7281) CTTTCTTTCTTTCTTTCTCTCTGT SEQ ID NO 2(1940)	CITICIT	TCTTTCTTTC	OTTCTCTGTCC.	CCTTTCTTTCTT	CCTTTCTTTC	TTTCTGCCT.	CTICCTITCTTTCTGCCTTTCTTTCTCTTCTTTCTCTTTCTCTTTCTCTTTCTCT	TGTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	TCTTTCTTTCCTTCTTTT	T T T T T T T T T T T T T T T T T T T
SEQ ID NO 15 (558) SEQ ID NO 16 (1)										
SEQ ID NO 17 (367) - Consensus(7281)										

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Section 82	GGTCTCC GGTCTCC 	7553	H H H C O D D C G C D D C D C G C H H	Section 84	7644	AGCTGC 	AGCTGC	AGCIGC
2780	A A G G	7540	TACAGITICAITATCITCCAGGCCTTICAITGGGTCAGGTTGGCATTITCGCTGCCCTITCAITATCTCCAGGCCTTTCAITGGGTTGGCATTITCGCTGCCCT	CICCAGGCCITICATIGGGTCAGGTIGGCATITCGCTGCCCI Section 84	7630	CTGGGCGTTTC	CITEGESCITIC	CIGGGCGITIC
7440	AGTGAAGCAC	7530	TGGGTCAGGT 10GGUCAGGT 1	TGGGTCAGGI	7620	GCAGCAGTTC GCAGCAGTTC 1 1 1 1 1 1 1 1 1 1	GCAGCAGTIC 	GCAGCAGIIC
7.430	TAAACAGGAA	7520	GGCCTTTCAT	GGCCTTTCAT	7610	CAGAATCTGC CAGAATCTGC	AAAAICAGAAICIGGGCAGCAGTICCIGGGCGIT	CAGAAICIGC
7400	STTAAAAGGT	7510	CATATCTCCA CATATCTCCA CATATCTCCA CATATCTCCA	TICATATCICCA	7600	16AA6AAAAT 16AA6AAAAT 11111111	GAAGAAAAI	IGAAGAAAA T
7440	CTTTTTCTA(7500	TTTACAGTTT(LI.	7590	ARAKOTCARG' ARAKOTCARG' 	GGAAAGAAAAACTCAAGIGAAG 	AAACTCAAG
	IAGATGAATG(7490	TATCTTCT 		7580	466888688878	466223 	4GGAAAGAAA
7300	CCATGTCTGTC	7480	STTCTTAATCA		7570	NGTGAAAATAA XGTGAAAATAA	4GTGAAAATAA 	AGTGAAAATAA
7380	TTAAGCAGAC	7470	TCTCCACACATC		7560	TGTGTGACA)	TGTGTGACAAG	TGTGTGACA
0757 (0767)	SEQ ID NO 11(7372) TTCCTTTTAAGCAGACCATGTCTGTT SEQ ID NO 2(1940)	(7463) 7463	SEQ ID NO 11(7463) AGTICATICTICCACATGITICTTAATICAT SEQ ID NO 2(1940)	Consensus(7463)	(7554) 7554 7560	SEQ ID NO 11(7554) TTATGTGTGTGTGAGAAGTGAAATAAGGAAAGAAAAACTCAAGTGAAGAAAATCAGGAATCTGCGCAGCAGTTCCTGGGCGTTTCAGCTGC SEQ ID NO 2(1989) TTATGTGTGTGTGACAAGTGAAATAAGGAAAGAAAAAACTCAAGTGAAGAAAATCAGAATCTGCGCAGCAGTTCCTGGGCGTTTCAGCTGC SEQ ID NO 13 (306)	SEQ ID NO 16 (51) TTATGTGTGTGACAAGTGAAATAA SEQ ID NO 17 (367)	Consensus(7554) TTATGTGTGTGACAAGTGAAAATAAGGAAAAGAAAAACTCAAGTGAAGAAAATCAGAATCTGCGCAGCAGTTCCTGGGGCGTTTCAGCTGC

Section 85	CCCAGCATCCATCTTCTTTGTTACACCCTGTGTGCATGACAGGCCCACCATTCATT	Consensus(/645) ITCCCACATCATCATCATCATCATCATTACATCATTATC Section 86 SEQ ID NO 11(7736) AGASCAAAGGATTCTCCCACTATTCTGGTTCACCTGCGAGGAGGAGGAGGAGGATTCTGCACGGATGACCTGCGTCACCTGGGAGGAGGAGGAGGATTCTCCCACTATTCTGGTTCACCCCCTACTTAGCCAGATATCTGCACGGATGACCTGCCTCACTGGGAGGAGGAGGAGGAGGAGGAGGATTCTCTCCCACTATTCTGGTTCACCCCCTACTTAGCCAGATATCTGCACGGATGACTTGCTCTCCCACTATTCTGGTTCACCTGGGAGGATTATAGAAGAATATCTGCACGGATGACTTGCTCTCCCACTATTCTGGTTCACCTCACTAGGAATATCTGCACGGATGACTTGCTCTCACTTAGCCAGATATCTGCACGGATGACTTGCTCTCACTTAGCCAGATATTCTGCACGGATGACCTGCTTAACTTAGCAAGAATATCTGCACGGATGACCTGCTTAACTTGGGAGGAGAGAATATCTGCACGGATGACCTGCTTAACTTAGCAAGAATATCTGCACGGATGACCTGCTTAACTTAGCAAGAATATCTGCACGGATGACCTGCTTAACTTAGCAAGAATATCTTGCACGGATGACCTGCTTAACTTAGCAAGAATATCTTGCACGGATGACCTGCTTAACTTAGCAAGAATATCTTGCACGGATGACCTGCTTAACTTAGCAAGAATATCTTGCACGGATGACCTGCTTAACTTAGCAAGAATATCTTGCACGGATGACCTTAACTTAGCAAGAATATCTTGCACGGATGACCTTAACTTAGCAAGAATATCTTGCACGGATGACCTTAACTTAGCAAGAATATCTTGCACGGATGACCTTAACTTAGCACGAAAACTAACT	GITCACCCCCTACTIAGCCAGATATACAAGAATATCTGCACGGATGACCTGCCTCACCTGGGAG Section 87 7860 7870 7880 7890 7900 7917	ATCGCACCAAGGACAGATCTCCCAGCAAGAATGACAGAAAAGACTAACTGCCCCCAAAATCTCCC ATCGCACCAAGGACTCTCCCAGCAAGAATGACAGAAAAGACTAACTGCCCCCAAAATCTCCC ATCGCACCAAGGACTCTCCCAGCAAGAATGACAGAAAAGACTAACTGCCCCCAAAATCTCCC ATCGCACCAAGGACAAGATCTCCCAGCAAGAATGACAAAAAGACTAACTGCCCCCAAAATCTCCC
0022	ACAGGCCC ACAGGCCC ACAGGCCC ACAGGCCC	ACAGGCCC 7810 SATGACCT	SAIGACCI 7900	OTAACTGC CTAACTGC CTAACTGC CTAACTGC
0,47	TGTGCATG	TGTGCATG/ 7800 TCTGCACG/ TCTGCACG/	 TCTGCACG(AGARARGA(AGARARGA(
0077	CCCAGCATCCATCTTGCTCATCTTACACCTGT CCCAGCATCCATCTTGCTCATCTTACACCTGT CCCAGCATCCATCTTGCTCATCTTACACCTGT CCCAGCATCCATCTTGCTCATCTTACACCTGT	TTACACCCTG 7790 ATACAAGAIA ATACAAGAAIA ATACAAGAAIA		SCAAGAATGAC SCAAGAATGAC
2600	0176010AT	7780 7780 FAGCCAGAT FAGCCAGAT FAGCCAGAT FAGCCAGAT FAGCCAGAT	 IAGCCAGAI 7870	SATCTCCCA SATCTCCCA SATCTCCCA SATCTCCCA SATCTCCCA
0007	CATCCATCTCC CATCCATCTCC CATCCATCTCC CATCCATC	7770 7770 CCCCCTACT CCCCCTACT CCCCCCTACT CCCCCCTACT CCCCCCTACT CCCCCCTACT CCCCCCTACT CCCCCCTACT CCCCCCTACT CCCCCCTACT CCCCCCTACT	CCCCCTACT	ACCAAGGACA(ACCAAGGACA(
01.01		TY60 TY60 TICTEGITCA TICTEGITCA TICTEGITCA TICTEGITCA		TTACTATCGC TTACTATCGC TTACTATCGC TTACTATCGC TTACTATCGC TTACTATCGC
0000	CACCTGCCTCAT	T750 T750 GICCGACIA CICCCACIA CICCCACIA CICCCACIA	 CICCCACIA 7840	CAGATTCCA CAGATTCCA
	(7645) TTCCCACAICACC (2080) TTCCCACAICACC (306)	Consensus(7645) ITCCCACATCACCTGCCTCATCAAGG (7736) 7736 7750 7750 7750 DID NO 11(7736) AGAGGAAAGGCTCTCCCACTATTCTG DID NO 13 (306)	OID NO 17 (367)	DID NO 11(7827) CTCAGAGGAGCTCAGATTCCATTACT OID NO 2(2262) CTCAGAGGAGCTCAGATTCCATTACT DID NO 13 (306)
[\ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \	SEQ ID NO 11(7645) TTCCCACATCACCTGCCTCATCAAGG SEQ ID NO 2(2080) TTCCCACATCACCTGCCTCATCAAGG SEQ ID NO 13 (306)	CONSENSUS (7645) TICCCACAICACCIGCCICAICAAGC (7736) 7736 7750 7750 SEQ ID NO 11(7736) AGASCAAAGGCICICCCACIAITCIG SEQ ID NO 13 (306)	SEQ ID NO 17 (367) Consensus(7736) AGA (7827) 7827	SEQ ID NO 11(7827) CTCAGAGGAGCTCAGATTCCATTACT SEQ ID NO 2(2262) CTCAGAGGAGCTCAGATTCCATTACT SEQ ID NO 13 (306)

SEC ID NO 13 (308) SEC ID NO 15 (308) SEC ID NO 16 (308) SEC ID NO 16 (308) SEC ID NO 17 (307) SEC ID NO 18 (308) SEC ID	SEC ID NO 11 (1918) FICCAAAACAGGGGTTTTTTATTCTCTCCAAGAACCAGGTTTCGCTCACCTCTTTAAGGACCTGGAAACAGGGCCATTTCAGCT SEC ID NO 13 (306) SEC ID NO 15 (386) SEC ID NO 15 (386) SEC ID NO 15 (386) SEC ID NO 15 (387) SEC ID NO 16 (415) FICCAAAACACAGGTTCTCTTAATTCTCCCAAGAACCAGGATGTGTCTCACCTCTCTAAGGACCTGGAAACAGGCCATTTCAGCT SEC ID NO 17 (387) SEC ID NO 17 (387) SEC ID NO 18 (389) SEC ID NO 19	(7918) 7918	7918	7930	7940	7950	7960	0262	7980	7990	
17 (367) 1.1. 1.2	16 (415)	0 11(7918) 10 2(2353) 0 13 (306) 15 (558)	TTCCAAAA TTCCAAAA	CACAGITCTC CACAGITCTC 	TTAATTCTCC TTAATTCTCC 	CAAGAAACCA(Caagaaacca(SAATGTGACT SAATGTGACT 	00000000000000000000000000000000000000	TCTAAGGACC TCTAAGGACC	TGAAAACAACII TGAAAACAACT	CCCCATTCX CCCCATTTCX CCCCATTTCX CCCCATTTCX
1000 1000 1	1000 1000	O 16 (415)	TTCCAAAA	CACAGTTCTC		CAAGAAACCA	SAATGTGACT	GCTCACCTC	TCTAAGGACC	TGAAAACAACI	CCCWIIIC
8009 8020 8020 8030 8040 8050 8060 8070 8080 8099	8020 8020 8030 8040 8050 8050 8080	nsus(7918)	TICCAAAA	CACAGIICIC	TTAATTCTCC	 CAAGAAACCA(SAATGTGACT	GCTCACCIC	TCTAAGGACC	TGAAACAACT	GGCCATITCA Secti
0.1(8009) ATTTABATCAACTITABABAATCCAACCGCCAAATATTABACCATTTTGGTTGGATAACATAAC	0.11(8009) ATTTAAATCAACTITAAAAAATCCAACGGCGAAATATTAAACCATTTTGGTTGG	(8008)	8008	8020	8030	8040	8050	8060	8070	8080	
(8100) 8100 8110 8120 8130 8140 8150 8150 8150 8150 8190	Section 50 Sec	713 (306) 715 (558) 716 (506) 717 (367)	ATTTAAAT:	CASCTTTAAA	AAATCCAACCC	000	INANCATT.		TGATARCATA		
(8100) 8100 8110 8120 8120 8130 8140 8150 8150 8170 8170 8180 8170 8170 8180 8170 8180 8170 8180 818	(8100) 8100 (8100) 8100 (8100) 8100 (8100) 60TAGGTGCAAAAAAAAAAAAAAAAATACTTCTAATCAGGTCAACTCTAGGGATTCTAAATTTACTCATATTCTCAAAGAAA (92.2535) 6CTAGGTGCAAAAATGGAAAAAAAAAATACTTCTAATCAGGTCAAATCTACTCTACTTTAGGATTTTACTCATATTCTCAAAGAAA (93.2535) 6CTAGGTGCAAAAATGGAAAAAAAAAAAAATCAAGTCAAATGACTCTACCTTTGGGATTCTAAATTTACTCATATTCTCAAAGAAA (93.2535) 6CTAGGTGCAAAAAAAAAAAAAAAAATCAAGTCAAATGACTCTACCTTTGGGATTCTAAATTTACTCATATTCTCAAAGAAA (93.7) 6CTAGGTGCAAAAATGGAAAAAAAAAATCAAGTCAAATGACTCTACCTTTGGGATTCTAAATTTACTCATATTTCTCAAAGAAA	(enno)snsı	ALLIAAAL	CAACIIIAAA	AAAICCAACC	CCAAAAIAI	IAAACCALLI	1 GG L L GG A A	IGALAACALA	ACIAACCIGCI	GACAGCIGCI
013 (306)	013 (306)	(8100) O 11(8100) VO 2(2535)	STASGIG GCTASGIG	SAAAAATGGA SAAAAATGGA	8120 AAAAAAAATAC AAAAAAAATAC	STICTAATCA(814U SGICAAAICA SGICAAAICA	SISU CICIACCIT CICIACCII	S15U TGGGATTCTA TGGGATTCTA	8170 AATITACICAI AATITACICAI	SISU ATTOTOAAAK ATTOTOAAAK
	0 17 (367)	O 13 (306) O 15 (558) O 16 (597)					SOICAAATCA	日 日 日 日 日 日 日 日 日 日 日 日 日 日 日 日 日 日 日			

Section 91 8281	CCAAT CCAAT	T	AATCAAT Section 92	8372	VIIOS VIIOS		AAATTCA Section 93	8463	01011111111111111111111111111111111111	- D - E - E - E	TICIC
Sec 8270	GACATTAA GACATTAA 	GACATTTAR	GACATTTAAT	8360	Tagarggaa? Tagarggaa?	CITITACAAICCAGACIAIAGAAGGAAAIICA	TAGAAGGAAF Sec	8450	ATGCCTGTT	-1 -1 -5 -1	CIGII
8260	TICABAICT TICABAICI	TICARATOTT	CITCAAAICI	8350	VAICCAGACT/	.ATCCAGACTA	AATCCAGACTA	8440	AACGGAAGIT AACGGAAGIT	 lacegaagiti	AACGGAAGTTI
8250	IEQ ID NO 11(8191) TATATTCAGTCATAGTGGGGAAAATAGGATTATTCCTTTAGCTCGATAAGCAACTTCTTCCTTC		AGGATTATICCTITAGCICGATAAGCAACCAGAAGIICTICCTICAAAICTIGACAITTAAICAA Section 92	8340	TTCCTATGAAGCTATCTCTGCCTGAAGGATTTTCTTTTACAATCCAGACTATAGAAGGAAATTCA TTCCTATGAAGCTATCTCTGTGCAAGGATTTTTCTTTTACAATCCAGACTATAGAAGGAAATTCA	TITCLL	TICCTATGAAGCTATCICTGCCTGAAGGATTTTTCTTTTACAATCCAGACTATAGAAGGAAATTCA Section 93	8430	SEQ ID NO 11(8373) CAACCTGGACTTTCACCTCCATTGGTCAGAGTTTTACTGACCAATTCCCACCTCGCCTTACACCGAAGGTTTATGCCTGTTTTCTC SEQ ID NO 2(2808) CAACCTGGACTTTGACTCATTGGTCAGAGTTTTACTGACCAATTCCCACCTCTGCCTTACACGGAAGTTTATGCCTGTTTTCTC SEQ ID NO 13 (306)	SEQ ID NO 15 (558)	ONS (1987)
8240	TAAGCAACCA TAAGCAACCA	 TAAGCAACCA	TAAGCAACCA	8330	CTGAAGGATT CTGAAGGATT	TICCTATGAAGCTATCICTGCCTGAAGGAITTIT	CTGAAGGATT	8420	CCCACCTCTG CCCACCTCTG 	CCCACCTCTG	CCCACCICIG
8230	TTTAGCTCGA TTTAGCTCGA		TTTAGCTCGA	8320	CIATOTOTGC	O	CTATCTCTGC	8410	CIGACCAAIT CIGACCAAII 		CIGACCAAIT
8220	GGATTALTCC GGATTALTCC 		GGATTATTCC	8310	TCCTATGAAG TCCTATGAAG		TCCTATGAAG	8400	CAGAGTTTTA CAGAGTTTTA 		CAGAGITITA
8210	GGGGAAATA GGGGAAAATA 		GGGGAAAATA	8300	GAAACTGTT GAAAACTGTT	GAAAACTGTT	GAAAACTGTT	8390	CTCCATTGGT CTCCATTGGT 	CICCALIGGI	CICCATIGGI
8200	SEQ ID NO 11(8191) TATATTCAG TCATAGTGGGGAAAAT SEQ ID NO 2(2626) TATATTCAG TCA TAGTGGGGAAAAT SEQ ID NO 13 (306)	SEQ ID NO 15 (558)SEQ ID NO 16 (688) TATATICAGICATAGIGGGGAAAAT SEQ ID NO 17 (367)	AG	8290	SEQ ID NO 11(8282) CAGAAATTGATTTTTTGGAAAACTGT SEQ ID NO 2(2717) CAGAAATTGATTTTTTGGAAAACTGT SEO ID NO 13 (306)		Consensus(8282) CAGAAATTGATTTTTGGAAAACTGT	8380	SEQ ID NO 11(8373) CAACCTGGACTTTCACCTCCATTGG SEQ ID NO 2(2808) CAACCTGGACTTTCACCTCCATTGG EQ ID NO 13 (306)	GGACTTICAC	GGACTTTCAC
(8191) 8191	(8191)	SEQ ID NO 15 (558) SEQ ID NO 16 (688) TATAITCA SEC ID NO 17 (362)	(8191) TATATI	(8282) 8282	SEQ ID NO 11(8282) CAGAAATT SEQ ID NO 2(2717) CAGAAATT SEO ID NO 13 (306)	SEQ ID NO 15 (558) SEQ ID NO 16 (779) CAGARATE SEQ ID NO 17 (367)	(8282) CAGAAA	(8373) 8373	SEQ ID NO 11(8373) CAACCTGGACTTT SEQ ID NO 2(2808) CAACCTGGACTTT SEQ ID NO 13 (306)	SEQ ID NO 15 (558) SEQ ID NO 16 (870) CAACCTGG SEO ID NO 17 (367)	(337) (8373) CAACCI
	SEQ ID NO 11(8191) TATA SEQ ID NO 2(2626) TATA SEQ ID NO 13 (306)	SEQ ID NO 15 SEQ ID NO 16	Consensus		SEQ ID NO 11- SEQ ID NO 2/ SEO ID NO 13	SEQ ID NO 16 SEQ ID NO 16 SEQ ID NO 16	Consensus		SEQ ID NO 11 SEQ ID NO 2 SEQ ID NO 13	SEQ ID NO 15 SEQ ID NO 16 SEO ID NO 17	Consensus

Section 97	8810 8827	EQ ID NO 11(8737) GICCAGGI CITATACAGCI CITATACACCCITI GIA TAACATGI CACGAATITCAGGGAICITTCAGIGA ICITAAGI CA SEQ ID NO 2(3172) GICCAGGI CIGI CITACAGCI CITATACACCCITI GIA I AACAGGAATI CAGGGAICI TOAGI GAGGI CA EQ ID NO 13 (306)	CAGCATAAAGGGATCITCAGIGAICIAAGICA	GTATATACACCCTTTGTATAACATGTCACGAATTCAGCATAAAGGGATCTTCAGTGATCTAAGTCA Section 98	8900 8918	EQ ID NO 11(8828) GGGGTCAGCAACCTTTTCTAAAAGGACCAAATAGTAATATTTCAGGCTTTGTGGACCCTATGGTCTCTATCATAACTGTTCAAATCACCA SEQ ID NO 2(3263) GGGCTCAGCAACCTTTTCTAAAAGGACCAAATAGTAATATTTCAGGCTTTGTGGACCCTATGGTCTCTATCATAACTGTTCAAATCACCA FO ID NO 13 (306)	CINTORIANCIGIIONANICACCA	Consensus(8828) GGGGTCAGCAACCTTTTCTAAAAGGACCAAATAGTAATATTTCAGGCTTTGTGGACCCTATGGTCTCTATCATAACTGTTCAAATCACCA Section 99	6006 0668	AAATATAAACTAACGAATGTGGCTGTTTTTATGGGATTTTTTTT	GITTIAISGGATTITITITAACICITTATITACAAAAGCAG
	8800	AGCATAAAGGG AGCATAAAGGG	AGCATAAAGSC	AGCATAAAGGG	8890	ATGGTCTCTA ATGGTCTCTA:	ATGGTCTCTA	ATGGTCTCTAT	8980	TITITITA TITITITA 	TTTTTTTAE
	8790	GTCACGAATTC GTCACGAATTC	CACGAATT	GICACGAAIIC	8880		 TTGTGGACCCT	TIGIGGACCCI	8970	AAATATAAASTAASSAATGTGGSTSTITTATSSGATTITTIT AAATATAAASTAASSAATSTGGSTSTIITATSGGATTITTT 	GTTTTAIGG9
	8780	TGTATAACAT	TGTATAACATGT	ITGTATAACAT	8870	EATTCAGGCT		FATTTCAGGCT	8960	CGAATGTGGCT CGAATGTGGCT	AATATAACTAACGAATGTGGCT
	8770	TATACACCCT TATACACCCT	TATATACACCCT	TATACACCCT	8860	CAAATAGTAA CAAATAGTAA 		CAAATAGTAA	8950	TATAAACTAA(TATAAACTAA(
	8760	CTCTAACGTA CTCTAACGTA	CICIAACGIA	CICTAACGIA	8850	TAAAAAGGAG TAAAAAGGAG		TAAAAAGGAC	8940	ATAAGCAAAA ATAAGCAAAA	eg
	8750	CTGTCTACAG CTGTCTACAG	CTGTCTACAG	CIGICIACAG	8840	CAACCTTTTC	CARCCITITC	CAACCITITC	8930	AAAAGGAGCC AAAAGGAGCC 	AAAAGGAGCC
	(8737) 8737	SEQ ID NO 11(8737) GTCCASGTCTGTCTACAGGCTCTAACGTATATACACCCTTT SEQ ID NO 2(3172) GTCCAGGTCTGTCTACAGGTCTAACGTATATACACCCTTT SEQ ID NO 13 (306)	SEQ ID NO 16(1234) GICCAGGICTGICTACAGCICTAACG SEQ ID NO 17 (367)	Consensus(8737) GICCAGGICIGICIACAGCICIAAC	(8828) 8828	SEQ ID NO 11(8828) GGGSTCASCAACCTTTCTAAAASGACCAAATAGTAATATTTCAGGCTTTGTGGACCCTATGGTCTCTATCATAACTGTTCAAATCACAA SEQ ID NO 2(3263) GGGSTCAGCAACCTTTCCTAAAAGGACCAAATAGTAATTTCAGGCTTTGTGGACCCTATGGICTCTATCATAACTGTTCAAATCACA SEO ID NO 13 (306)	SEQID NO 15 (588) SEQID NO 15 (1325) GGGGTCAGCAAACCTTTTCTAAAAAGGACCAAATAGTAATATTTCAGGCTTTGTGGACCCTATGGTCT SEQID NO 17 (367)	Consensus(8828) GGGGTCAG	(8919) 8919	SEQ ID NO 11(8919) TGTAGTGTAAAAGGAGCCATAAGCA SEQ ID NO 2(3354) TGTAGTGTAAAAGGAGCCATAAGCA SEQ ID NO 13 (306)	SEQ ID NO 15 (336)

(9010)	010 9020	0006	9040	9050	0906	9070	0806	0606 S	Section 100 9100
SEQ ID NO 11(9010) GIGGCAGAICAGAACTCACTTAIGGCCCATAGITCICIGACCCCIGAGAAAATCITRIRITIATGGACAACAITIAGACTGIGACTGIGACT SEQ ID NO 2(3445) GIGGCAGAICAGAACTCACTTAIGGCCCATAGITCICIGACCCCTGACCTGA	TGGCAGATCAG TGGCAGATCAG	AACTCACTTATGC AACTCACTTATGC	GCCATAGITC	GCCATAGITCTCTGACCCCTGACCTGAGAAATCTTATATTT	ACCTGAGAAA	ATCTERTRE ATCTERTAL	TTATEGACAA ITATGGACAA	AIGGACAACAITIAGACIGIGACI Aiggacaacaiitagacigigaci	GTGACT
SEQ ID NO 15 (558)	TGGCAGATCAG		SCCATAGTTC			ATCTTATAT			 GIGACI
SEQ ID NO 17 (367) Consensus(9010) GTGG	TGGCAGATCAG	ID NO 17 (367)	GCCATAGITC	GCCATAGTICTCTGACCCTGACCTGAGAAATCTTATATTTATGGACAACATTTAGACTGTGACT	ACCIGAGAAA	ATCTTATAT	 ITATGGACAA	 CATTTAGACI S	TGTGACT
(9101) 9101	101 9110	9120	9130	9140	9150	9160	9170	9180	9191
SEQ ID NO 11(9101) TGCCAAGTAAGAACAAGAAGCTCTG SEQ ID NO 2(3536) TGCCAAGTAAGAACAAGAAGCTCTG SEO ID NO 49 (2008)	GCCAAGTAAGA GCCAAGTAAGA	ACAAGAAGCICIC ACAAGAAGCICIC	TCAACTGAAG	TCAACTGAAGGTCAAGGCTGGAGTTCTGAAAGCAAAGAGCTGTCTGGTGTTAATGATAAGTGAAAT TCAACTGAAGGTCAAGGCTGGAGTTCTGAAAGCAAAGAGCTGTCTGGTGTTAATGATAAGTGAAAT	AGTICIGAAA	GCAAAGAGC GCAAAGAGC	rercrearer Fercrearer	Taatgataag Taatgataag	IGAAAT IGAAAT
SEQ ID NO 15 (500)									
SEQ ID NO 17 (367) Consensus(9101) TG	GCCAAGTAAGA	JID NO 17 (367)	TCAACTGAAG	TCAACTGAAGGTCAAGGCTGGAGTTCTGAAAGCAAAGAGCTGTCTGGTGTTAATGATAAGTGAAAT Section 102	AGTTCTGAAA	GCAAAGAGC	IGTCTGGTGT	TAATGATAAG	GTGAAAT Section 102
(9192) 9192	192 9200	9210	9220	9230	9240	9250	9260	9270	9282
SEQ ID NO 11(9192) AGTTARAGTTAGRAGATCCCAGTTA SEQ ID NO 2(3627) AGTTARAGTTAGRAGATCCCAGTTA SEQ ID NO 13 (306)	GTTAAAGTTAGA GTTAAAGTTAGA 	AAGATCCCAGTTA AAGATCCCAGTTA	TAAGAAGCAC TAAGAAGCAC	TAAGAAGCACAAAAATAATGACCATAGACTCCTGAACAAGAATGTCTGGACTTCTGGCTTAGGCA TAAGAAGCACAAAGAATAATGACCATAGACTCCTGAACAAGAATGTCTGGACTTCTGGCTTAGGCA 	ACCATAGACT ACCATAGACT	CCTGAACAA CCTGAACAA	GAATGTOTGG SAATGTOTGG	ACTTCIESC:	TAGGCA TAGGCA
SEQ ID NO 15 (538) SEQ ID NO 16(1689) AGTIAAAGITAGAAGATCCCAGTIAI	 GTIAAAGIIAG	 AAGATCCCAGII?	 taagaagcac	 aagaagcacaaaaaaataaigaccatasaciccisaacaabaisiciggactictiagga	ACCATAGACI	CCTGAACAA	 baatsicies	ACTICIGGCI	TAGGCA
SEQ ID NO 17 (367) Consensus(9192) AGITAAAG	GITAAAGITAG	JID NO 17 (367)	TAAGAAGCAC	 Taagaagcacaaaagaataatgaccatagactcctgaacaagaatgtctggacttctggcttaggca	ACCATAGACT	CCTGAACAA	GAATGTCTGG	ACTICIGGCI	TAGGCA

ABABGTAT Sabagtat 	M		9458	
4748 4784 4781	 aataaa	 AATAAAAGTA	U)	CCCATGTCAAGCACATAGAATAGGGCCCAGCCTATATTAATTIATCAATAAATGCCAG CCCATGTCAAGCACATAGGGCCCAGCCTATATTAATTTATCAATAAATGCCAG CCCATGTCAAGCACATAGAATAGGGCCCAGCCTATATTAATTTATCAATAATGCCAG
caatcaacat Laatcaacat 		AATGAAGATAA	9440	TIAATITAT TUAATITAT TTAATITAT
CTTATCATTA CTTATCATTA 	CITAICATIA	CITAICAITA	9430	CCCASCCTATA CCCASCCTATA CCCASCCTATA CCCASCCTATA
CCECCATITI		CCICCAIIII	9420	AGAATAGGGC AGAATAGGGC
TCTCTCCAGG TCTCTCCAGG	TCTCTCCAGG	 ICICICCAGG	9410	TCAAGCACAT TCAAGCACAT
		 AGIIACCIAA	9400	CTAACCCATG
9700AGGCCA. 3700AGGCCA. 11111111111111111111111111111111111		SICCAGGCCA	9390	ATAAACTGAG
GTTGTATG GTTGTATG(GIIGIVIG	GITGIAIG(9380	CIGTAAGAA CIGIAAGAA CIGTAAGAA
NO 11(9283) CTCTT D NO 2(3718) CTCTT NO 13 (306)	NO 15 (558) NO 16(1780) CTCTT NO 17 (367)	sensus(9283) CICII	(9374) 9374	SEQ ID NO 11(9374) GAGAGCTGTAAGAATAAACTGAGCTAACCCATGTCAAGCACATAGGGCCCAGCCTATATTAATTIATCAATAATGCCAGGSCCAGGCCTATATTAATTIATCAATAAATGCCAGGSCCAGGCCCAGCCTATATTAATTTAAT
	GTTGTATGGTCCAGGCCAAGTTACCTAATCTCTCAGGCCTCCATTTTCTTATCATTAAATGA GTTGTATGGTCCAGGCCAAGTTACCTAATCTCTCAGGCCTCCATTTCTTATCATTAAATGA 			

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91	ACAAAAAG 1CAAAAAG 1CAAAAAG 1	Section 2	AAACCAGG	AAACCAGG — Section 3	273 AGATGGC AGATGGC
80	TTGAATAAAACAAAAAG 	170	TTCAGACTIA TTCAGACTIA	TICAGACIIA	250 260 273 TCCTGGTTCTCCAGCTTGCAGATGGC TCCTGGTTCTCCAGCTTGCAGATGGC
70	GTCGAAAGCT GTCGAAAGCT	160	TGGATGTGAGTGGGCCTTCAGACTTAAACCAGG GGATGTGAGTGGGCCTTCAGACTTAAACCAGG TGGATGTGGGCCTTCAGACTTAAACCAGG	GGATGTGAGTGGCCTTCAGACTTAAACCAGG	ZEO TCCTGGTTC TCCTGGTTC TCCTGGTTC
90	CATCCAATCTG	150	CCTTGGATG	GGATG	240 CTGCCAGGT CTGCCAGGT CTGCCAGGT
90	(1) ATTIGAATIGGIGAACTTAGIAAAGCAGACGGCTCTCACCAATAAGGGCAGGCATCATCCATC	140	CTIGATCTAGTATATCATCTTCTCTGCCCTTGGATGTGAGTGGGCCTTCAGACTTAAACCAGG 		183) 183 190 200 210 220 230 240 250 260 273 183) AGTTACACCTTTGGCTTCTCTGGTTCTTTTGGACTTGGACTTGGATTACACTGCCAGGTTTCCTGGTTCTCCAGGTTGCAGATGGC (33) AGTTACACCTTTGGTTCTCAGTTCTTTGGACTTGGACTTGGACTTGCAGGTTTCCTGGTTCTCCAGGTTGCAGATGGC (4)<
40	CTCACCAATAAG 	130	CTAGTATATCATCT	 	Z20 TGGACTIGGA TGGACTIGGA TGGACTIGGA TGGACTIGGA TGGACTIGGA
30	CAGACGGCTC CAGACGGCTC CAGACGGCTC	120	TICTIGAICT TICTIGAICT TICTIGAICT		SEQ ID NO 11 (183) AGTTACACCTTTGGCTTCCCTGGTTCTCAGTTCTTTGGA SEQ ID NO 4 (33) AGTTACACCTTTGGCTTCCCTGGTTCTCAGTTCTTTGGA SEQ ID NO 13 (183) AGTTACACCTTTGGCTTCCCTGGTTCTCAGTTCTTTGGA SEQ ID NO 14 (1)
8	(1) ATTTGAATTGGTGAACTTAGTAAAGCAGACGGCT (1)	110	(92) AGGAAGGGAAATTTGCTTCTTTCTT (1)		SEQ ID NO 11 (183) AGTTACACCTTTGGCTTCCCTGGTTC SEQ ID NO 4 (33) AGTTACACCTTTGGCTTCCCTGGTTC SEQ ID NO 13 (183) AGTTACACCTTTGGCTTCCCTGGTTC SEQ ID NO 16 (1)
10	AATTGGTGAA 	100	32) AGGAAGGGAAAATTTG (1)		190 CACCTTTGGC CACCTTTGGC CACCTTTGGC CACCTTTGGC
(1) 1	(1) ATTTGZ (1) (1) ATTTGZ (1) (1)	(1)	(92) AGGAAG (1) (92) AGGAAG (1) (1)	(92)	(183) 183 (183) AGTIAK (183) AGTIAK (1) (1) (1) (183) AGTIAK
	SEQ ID NO 11 SEQ ID NO 4 SEQ ID NO 13 SEQ ID NO 16 SEQ ID NO 15 SEQ ID NO 15	Consensus	SEQ ID NO 11 SEQ ID NO 4 SEQ ID NO 13 SEQ ID NO 13 SEQ ID NO 16 SEQ ID NO 16	Consensus	SEQ ID NO 11 SEQ ID NO 44 SEQ ID NO 13 SEQ ID NO 13 SEQ ID NO 16 SEQ ID NO 15 SEQ ID NO 15 Consensus

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SEOID NO 4 (124) AGANCATCGGGGCTTCTTGGCCTCCATAATTGT	(274) 274	280	290		310	320	330	340	350	Section 4 364
Section Sect	SEQ ID NO 1 (274) AGA SEQ ID NO 13 (274) AGA SEQ ID NO 16 (1) SEQ ID NO 15 (1) SEQ ID NO 17 (1) Consensus (274) AGA	TCATGGGAN TCATGGGAN TCATGGGAN TCATGGG			31GAGICAAT		TIACALALCO	AG 11 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	IGC111444C441166	4 4 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
(365) GGITCTGAGAAATGCATTGTTAAGTGATTTCATCATTGTGCAAACATCATAGAGTGTAACTACACAAACCTGGACAGCATAGACTACTACTACTAGAGTGTACTACTAGAGAAATGCATTGTTAAGTGTTTCATCATTGTGCAAACATCATAGAGTGTAACTACTACTAGAGAAATGCATTGTTAAGTGTTTCATCATTGTGCAAACATCATAGAGTGTAACTACTACTACTAGAGTGTACTACTAGAGAAATGCATTGTTAAGAGTTTTCATCATTGTGCAAACATGGACAAACCTGGACAGCATACTACTACTACTACTACTACTACTACTACTACTACTA	(365) 365	370	380	390	400	410	420	430		ection 5 455
(456) 456 470 480 490 500 510 520 530 (456) CATCTAGGCTACATGTAACCTCATGATAAGTATGTATAACATCATGATAAGTATGTAT	1 (365) GGTT 4 (215) GGTT 3 (306) 6 (1) 7 (1) s (365)	TCTGAGAA! TCTGAGAA!	ATGCATTGTTA ATGCATTGTTA ATGCATTGTTA ATGCATTGTTA	AGTGATTTCA: AGTGATTTCA:	ICATIGIGCA ICATIGIGCA ICATIGIGCA ICATIGIGCA	AACATCATAGAACATCATAGAACATCATAGAACATCATAGAACATCATAGAACATCATAGAACATCATAGAACAACAACAACAACAACAACAACAACAACAACAACAA	GTGTAACTAC	ACAAACCTGG ACAAACCTGG	ACAGCATAGACTA ACAGCATAGACTA 	TACA TACA TACA TACA
(306)	(456) 456 1 (456) CATO 4 (306) CATO	CTAGGCTAC	470 ATGGTGTAGC	480 TIGIAACCICA	490 ATGATAAGTA ATGATAAGTA	500 IGTATAACATO IGTATAACATO	510 ATGATAAGTA ATGATAAGTA	520 IGTATGTATC IGTATGTATC	530 TACCATATCTAAA TACCATATCTAAA	546 GTAG
	9									

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729 740 750 IIGACICIAITICAAAAITIAIGGI	(638) ACTGTATACGCACACATACACACACACACAATATACTATTGGTTCTTT (488) ACTGTATACGCACACATACAATATACTATTGGTTCTTT (306)	(638) 638 650 660 670 670 710	AATCITATGGGATCACCATCATATATGCAATCCTITGTAGACTGAAATGTCATTGTGTAGTGCATG ACACACAAATATACTATTGGTTCTTTTTCTCTGAAGAGCCCTAATACAATATGTTATACATTTATA ACACACAAATATACTATTGGTTCTTTTTCTCTGAAGAGCCCTAATACAATATGTTATACATTTATA ACACACAAATATACTATTGGTTCTTTTTCTCTGAAGAGCCCTAATACAATATACATTTATA ACACACAAATATACTATTGGTTCTTTTTCTCTGAAGAGCCCTAATACAATATACATTTATA ACACACAAATATACTATTGGTTCTTTTTCTCTGAAGAGCCCTAATACAATATACATTTATA ACACACAAATATACTATTGGTTCTTTTTCTCTGAAGAGCCCTAATACAATATGTTATACATTTATA ACACACAAATATACTATTGGTTCTTTTTCTCTGAAGAGCCCTAATACGATTATATACATTTATA ACACACAAATATACTATTGGTTCTTTTTTCTCTGAAGAGCCCTAATACAATATGTTATACATTTATA ACACACACAAATATACTATTGGTTCTTTTTTTTTT	710 AATACAATATG AATACAATATCAATATG AATACAATATCAATATG AATACAATATCAATATG AATACAATATCAATATCAATATCAATATCAATATCAATATCAATATCAATATCAATATCAATATCAATATCAATATCAAT	CTTTGTAGACTGAAATGTCAT	690 1 T T T T C T C T C T T T T T T C T C T	680 1 ATT GGTTC 1 TATT GGTTC 1 TATT GGTTC 1 TATT GGTTC 1 TATT GGTTC 1 TATT GGTTC	######################################	1GGTATAATC 1TGGTATAATC 1	AGTAAAATA AGTAAAATA	SEQ ID NO 11 (547) AAAAGGTACAGTACAATATGGTATAATCTTATGGGATCACCATCATATATGCAATCC SEQ ID NO 4 (397) AAAAGGTACAGTACAAAATATGGTATAATCTTATGGGATCACCATCATATATGCAATCC SEQ ID NO 13 (306)
SEQ ID NO 4 (579) TTGACTCTATTTCAAAATTTATGGTTTTTGGTGAACATATGTGGGGGCATAGGTGTGTGT	(729) 729 740 750 760 770 780 790 800 (729) TIGACICIATITICAAAATITIAGGGGGGGGGGGGGGGGG	GTATACGCACACATACAACACACAAATATACTATTGGTTCTTTTTCTCTGAAGAGCCCTAATACAATATGTTATACATTTACATTTTCTCTGAAGAGCCCTAATACAATATGTTATACATTTTCTTTTCTCTGAAGAGCCCTAATACAATATGTTATACATTTTTCTTTTTCTCTGAAGAGCCCTAATACAATATGTTATACATTTTTCTTTTTCTCTGAAGAGCCCTAATACAATATGTTATACATTTTTTCTCTGAAGAGCCCTAATACAATATGTTATACATTTTTTTT	CCTGCTGATGAAT	TGGGATAGTGT 	GTGTGTGAAC	.GGGCCATAG	TGTGGAGAT 	GTGAAACATA 	TATGGTTTTG	TTTCAAAATT 	(579) TTGACTCTA (306) (1)
650 660 670 680 710 GTATACGCACACACAAACAATATACTATTGGTTCTTTTTCTCTGAAGAGCCCTAATACAATATGTTATACATTTA GTATACGCACACACAACACACAAATATACTATTGGTTCTTTTTCTCTGAAGAGCCCTAATACAATATGTTATACATTTA	(638) 638 650 660 670 680 690 700 710		Section 8								(1) (1) (1) (547)
650 660 670 680 700 710 GTATACGCACACACACACACACACATATACTATTGGTTCTTTTCTCTGAAGAGCCCTAATACAATATACATTTA GTATACGCACACACACACACACACACACACATATACTATTGGTTCTTTTTCTCTGAAGAGCCCTAATACAATATACATTTA Section Sectio	Section 650 660 670 680 690 700 710		TGTGTAGTGCATG	14010144401	CTTTGTAGAC	TAIGCAAIC TAIGCAAIC	ACCAICAIA ACCATCAIA 	TTATGGGATC TTATGGGATC	TGGTATAATC TGGTATAATC	AGTAAAAATA AGTAAAAATA 	(397) AAAAGGTAC (397) AAAAGGTAC (306)

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	(820) 820	830	840	850	098	870	088	990	006	Section 10 910
SEQ ID NO 11 (820) GG SEQ ID NO 4 (670) GG SEQ ID NO 13 (306) SEQ ID NO 16 (1) SEQ ID NO 15 (1) SEQ ID NO 17 (1) Consensus (820)	1 (820) GGGTG 4 (670) GGGTG 3 (306) 5 (1) 7 (1) 8 (820)	SEQ ID NO 11 (820) GGGTGGGAGGCATCATTTGGGACAAGCCCCAGGGCATCAGATATCAAGAGCTCAACAAGAGCACTTTATGGCAAAACCTCCCACA SEQ ID NO 4 (670) GGGTGGGAGGCATCATTTGGGACAAGCCCCACGAGGCATCACAAGAGCTCCACCACACACA	TTTGGGACAA(TTTGGGACAA(GCCCAGGGCA GCCCAGGGCA GCCCAGGGCA GCCCAGGGCA GCCCAGGGCA	CCCAGGGCATCAGCTTATAGATATCAAGAGCTCAACAAGAGCACTTTATGGCAAAACCTCCCACACACA	5ATATCAAGA 5ATATCAAGA 	GCTCAACAAG.	AGCACITIAIC AGCACITIAIC 	5GCAAAACCT 5GCAAAACCT 1	CCCACA
	(911) 911	920	930	940	950	096	970	086	066	1001
SEQ ID NO 11 (911) SEQ ID NO 4 (761) SEQ ID NO 13 (306) SEQ ID NO 16 (1) SEQ ID NO 15 (1) SEQ ID NO 15 (1) SEQ ID NO 17 (1)	SEQ ID NO 11 (911) AGACCT SEQ ID NO 4 (761) AGACCT SEQ ID NO 13 (306) SEQ ID NO 16 (1) SEQ ID NO 15 (1) SEQ ID NO 17 (1) SEQ ID NO 17 (1)	SEQ ID NO 11 (911) AGACCTCTCAGAAGTTGAGAAACTGCTAAAAGT SEQ ID NO 4 (761) AGACCTCTCAGAAGTTGAGAAACTGCTAAAAGT SEQ ID NO 13 (306)	GAGAAACTG(GAGAAACTG(GAGAAACTG(GAAACTG(GAAACTG(GAAACTG(GAAACTG(GAAACTG(GAAACTG(GAAACTG(GAAACTG(GAAACTG(GAAACTG(GAAACTG(GAAACTG(GAAACTG(GAAACTG(GAAACTG(GAAACTG(GAAACTGG(GAAACTGG(GAAACTGG(GAAACTGG(GAAACTGG(GAAACTGG(GAAACTGG(GAAACTGG(GAAACTGG(GAAACTGG(GAAACTGG(GAAACTGG(GAAACTGG(GAAACTGG(GAAACTGG(GAAACTGG(GAAACTGG(GAAACTGGG(GAAACTGGGGGAAACTGGGGGAAACTGGGGGAAACTGGGGGAAACTGGGGAAACTGGGGAAACTGGGGAAACTGGGGAAACTGGGGAAACTGGGGAAACTGGGGAAACTGGGGAAACTGGGGAAACTGGGAAACTGGGAAACTGGGAAACTGGGAAACTGGGAAACTGGGAAACTGGGAAACTGGGAAACTGAAACTGGAAACTGGAAACTGGAAACTGGAAACTGGAAACTGGAAACTGGAAACTGGAAACTGAAAACTGAAAACTGAAAACTGAAAACTGAAAACTGAAAACTGAAACTGAAACTGAAAACTGAAAACTGAAAAACTGAAAACTGAAAACTGAAAAAAAA	CTAAAAGTTT CTAAAAGTTT 		TATGACAGATGACATTT. TATGACAGATGACATTT	ATGGATAAAA ATGGATAAAA 	TATGACAGATGACATTTATGGATAAAATAGGGATTAGCAGGATTCTTTAAATA TATGACAGATGACATTTATGGATAAAATAGGGATTAGCAGGATTCTTTAAATA TATGACAGATGACATTTATGGATAAAATAGGGATTAGCAGGATTCTTTAAATA	2AGGATTCT7 2AGGATTCT7 1AGGATTCT7 1AGGATTCT7 1AGGATTCT7	ITAAATA
	(1002) 1002	1010	1020	1030	1040	1050	1060	1070	1080	1092
EQ ID NO 11 SEQ ID NO 4 EQ ID NO 13	SEQ ID NO 11(1002) CITITO SEQ ID NO 4 (852) CITITO SEQ ID NO 13 (306)	SEQ ID NO 11(1002) CTTTCGAACACTAACCTTCATTTCTACCAGGCAGTGGGGGCCCCAAGTGCAGGGCCATAGGAAGTACAAGTCTGGGAAGTACTAGGCTGCAC SEQ ID NO 44 (852) CTTTCGAACACTAACCTTCATTTCTACCAGGCAGTGGGGGCCCCAAGTGCAGGGCCATAGGAAGTACAAGTCTGGGAAGTACTAGGCTGCAC SEQ ID NO 13 (306)	CTTCATTTCT/	ACCAGGCAGT ACCAGGCAGT	GGGCCCCAAC GGGGCCCCAAC	9TGCAGGGCC 9TGCAGGGCC	ATAGGAAGTA ATAGGAAGTA	CAAGTCTGGG/ CAAGTCTGGG/ 	AGATACTAGO AGATACTAGO	CTGCAC
SEQ ID NO 15 SEQ ID NO 17	(1)									
Consensus(1002)	\$(1002)									

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AGAGAATCTGAAAAATAATAGAGTC AGAGAATCTGAAAAATAATAGAGTC	ACTGAAATGCAGTTTGGTATAATTATTGCCATGCATCATAATTCTAAATCATACTAGT ACTGAAATGCAGTTTGGTATAATTATTGCCATGCATCATAATTCTAAATCATACTAGT	CATACTAGT CATACTAGT Section 14 1274 TATAAATAC
(1184) 1184 1190 1200 1210 1220 1230 1230 1240 11(1184) GGTCAAATACTCTTCCTGAAAAACATTTTCTTGGTTTGAATTCTAAATAGTTG	1240 1250 1260 TGTTGTTGTGTCACCACTGAGCTTTTAAATTTGTTGTGGTCACCACTGAGCTTTTAAATTGTTGTGTCACCACTGAGCTTTTAAATT	1274 TATAAATAC TATAAATAC
OD NO 41(1184) GGTCAAATACTCTTCCCTGAAAAACATTTTCTTGGTTTGAATTCTAAATAATTG	TIGITGIGGICACCACTGAGCTITTAAAI TIGITGIGGICACCACTGAGCTITTAAAI	TATAAATAC TATAAATAC
SEQ ID NO 13 (306)		
Section 15 (1275) 1275 1280 1290 1300 1300 1310 1320 1320 1330 1340 1350 1350 1365 (1275) SECTION 1014(1075) 1275 1280 1350 1350 1350 1350 1365	1330 1340 1340 1350	1365 1365
SEQID NO 4(1125) ITTCAAGITICCATATITITATIACCIGITICCITAACAAACATIGAAATGATATIGGGAAACATICGGGTATACAGICCCSEQID NO 4(1125) ITTCAAGITICGGGTATACCAGAACATICGAGAACATICGGGTATACAGTCCCSEQID NO 43 (306)	CATGAAAATGATTATGGGAAACATTCGGG	AIACAGICC

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(1366) 1366	1380	1390	1400	1410	1420	1430	1440	Section 16 1456
SEQ ID NO 41(1366) SEQ ID NO 4(1216) SEQ ID NO 4(1216) SEQ ID NO 4(1216) SEQ ID NO 4(1216) SEQ ID NO 13 (306) SEQ ID NO 13 (306)	(GGACTCAGGT (GGACT	AAATACTTAG AAATACTTAG 	GGTATTTCAT GGTATTTCAT 	GGCCCTAGTC GGCCCTAGTC 	TTTGGGGTA(CCACATGTTT CCACATGTTT	CITTGGGGTACCACATGTTTCTTCTAAATCACAGATTCACACTTTGGGGTACCACACATTTCTTCTTCAAATCACAGATTCAATTCAAATCACAGATTCAAATCACAGATTCAAATCACAGATTCAAATCACAGATTCAAATCACAGATTCAAATCACAGATTCAAATCACAGATTCAAATCACAGATTCAAATCACAGATTCAAATCACAGATTCAAATCACAGATTCAAATCACAGAATCAAAATCACAGAATCAAAAACAAAAAAAA	AGATTCA AGATTCA
(1457) 1457	1470	1480	1490	1500	1510	1520	1530	1547
SEQ ID NO 11(1457) AAATCAAGAATGATAACCACAGTGATTGTGTAGACCAAAATTGCTTGC	GATAACACAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	11GATIGIGIA 11GATIGIGIA 11GATIGIGIA 11GATIGIA 11GATIA 11GATIA 11GATIA 11GATIA	GACAAATAA GACAAAATAA 	GTGAACCAAA GTGAACCAAA 	ATTGCTTGC ATTGCT ATTG	TCTGTCATT	GIGIAGACAAAATAAGIGAACCAAAATIGCIIGCIICIGICATICIAIGGAACCACIGAGAGITI GIGIAGACAAAATAAGIGAACCAAAATIGCIIGCIICIGICATICIAIGGAACCACIGAGAGITI	AGAGTTT AGAGTTTT AGAGTTTT AGAGTTTT AGAGTTTT
(1548) 1548	1560	1570	1580	1590	1600	1610	1620	Section 18 1638
SEQ ID NO 11(1548) TTACTTGTGCTTAAAATTTTGAATAGTAAAACAGAGTGTCAACTTCATGCTGGAATATT SEQ ID NO 4(1398) TTACTTGTGCTTAAAATTTTGAATAGTAAAACAGAGTGTCAACTTCATGCTGGAATATT SEQ ID NO 13 (306)	TAAAATTTTG TAAAATTTTG TAAAATTTTG	3AATAGTAAAA 3AATAGTAAAA 	CAGAGIGICA	ACTICAIGCI ACTICAIGCI 	GGAATATTT .GGAATATTT	TTGGCTHTHTHTHTHTHTHTHTHTHTHTHTHTHTHTHTHT	GTAAAACAGAGTGTCAACTTCATGCTGGAATAITITTTGGCTTTTTTAGACACAATTTTAAGTACATGGTAAAATGTAAAATGTAAAATGTAAAATGTAAAATGTAAAATGTAAAATGTAAAATGGTAAAAAA	STACATG STACATG STACATG

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(1639) 1639	1639	1650	,1660	1670	1680	1690	1700	1710	Section 19 1729
SEQ ID NO 11(1639) AAGTATTTTTACAAGACTAAGTAACATCACTGAAATTACAGCTTTCTTCTTTTAAAACTGGTATTTGTTATAAAACTAAAAGAGCGAATCA SEQ ID NO 4(1489) AAGTATTTTTACAAGACTAAGTAACATCACTGAAATTACAGCTTTCTTT	AAGTATTTI AAGTATTTT 	TACAAGACTA TACAAGACTA	AAGTAACATCAC AAGTAACATCAC 	CTGAAATTACZ CTGAAATTACZ	AGCTTTCTTC AGCTTTCTTC	ITTTTAAAACI ITTTTAAAACI 	GGTATTTGT	TCACTGAAATTACAGCTTTCTTCTTTTAAAACTGGTATTTGTTATAAAACTAAAGAGCGAATCA TCACTGAAATTACAGCTTTCTTTTTTAAAACTGGTATTTGTTATAAAACTAAAGAGCGAATCA 	GAGCGAATC GAGCGAATC
SEQ ID NO 15 (1) SEQ ID NO 17 (1) Consensus(1639)									Section 20
(1730) 1730	1730	1740	1750	1760	1770	1780	1790	1800	1810 1820
SEQ ID NO 11(1730) AGAAAAGCATAATTATTACTGATTATTACTGAAAAAGAAATGTACGGAATAGAAGGAGGAGGAGGAGGTTAACAAATGATCCAC SEQ ID NO 4(1580) AGAAAAGCATAATTATTACTGATTATTACTGAAAAAGAAATGTACGGAATAGAGGAGGAGGAGGTTAACAAATGATCCAC SEQ ID NO 13 (306)	30) AGAAAAGCAT 80) AGAAAAGCAT 06) (1) (1) (1)	ATAATTATTAC	CTGATTATTAC! CTGATTATTAC!	AGGATTATTA(AGGATTATTA(CTGAAAAAGA CTGAAAAAGA CTGAAAAAGA CTGAAAAAAAAAA	AATGTACGGAAAAATGTACGGAAAAATGTACGGAAAAAAAA	ATAGAGGAGGATATAGAGGAGGGAGGGAGGGAGGGAGGG	TACAGGATTATTACTGAAAAAGAAATGTACGGAATAGAGGAGGAAGGA	AATGATCCA AATGATCCA
(roor)	7007	000							Section
(1821) 1821 1830 1830 1840 1850 1870 1850 1860 1860 1870 1870 1880 1871 SEQ ID NO 11(1821) TUTGGGTGAAACACCAATAAGCCTGCTTCCAGGAAGTGCCTAAGACAGGGTGGGT	1821 TCTGGGTGT TCTGGGTGT	1830 TGAAAACACC TGAAAACACC	1840 Caataagccigc Caataagccigc	1850 CIICCAGGAA(CIICCAGGAA	1850 GIGCCIAAGA GIGCCIAAGA	1870 CAGAGCIGGCI CAGAGCIGGCI	TCAGCTTGCT(TCAGCT)	1850 1850 1860 1860 1870 1830 1831 1831 CAGGAGGAGGAGGAGGAGGAGGAGGAGGAAGGAAAC CIGCIICCAGGAAGIGCCIAAGACAGAGCIGGCICAGCIIGCIGGGICACAGCAIGIAAGGAAAC CIGCIICCAGGAAGIGCCIAAGACAGAGCIGGCICAGCIIGCIGGGICACAGCAIGIAAGGAAAC	1900 ATGTAAGGAAAC ATGTAAGGAAAC
SEQ ID NO 13 (306) SEQ ID NO 16 (1) SEO ID NO 15 (1)									
SEQ ID NO 17 (1)							 		
Consensus(1821)									

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Section 22	2030 2040 2050 2060 2070 2080 2093 ITATGIGAATTAACTITIGICAAATTTATTTTTCATAAATAACCCAAATATGIATACCACTATTA TTATGIGAATTAACTITTGICAAATTTATTTTTCATAAATAACCCAAATATGIATACCACTATTA	Section 24
1970 CCATGGGGAP	2060 ATTTTTCATA ATTTTTCATA	2150 AGTTAAGACTC
1960 TCCCATAGCC TCCCATAGCC	2050 TGTCAAATITAT TGTCAAATITAT 	Z140 TCTAACCCAA TCTAACCCAA
1950 AGATAGATAA AGATAGATAA 	2040 AATTAACTTT AATTAACTTT	2130 AGTTTAAATA AGTTTAAATA
1940 ICAGITGICC ICAGITGICC	2030 TCCTTTATGTG TCCTTTATGTG	SAGCICCIAA
1930 5CCACCATCC 	2020 FATGCTAAGT FATGCTAAGT 	2110 AGGAGAAACT AGGAGAAACT
1920 GGGCTACATC GGGCTACATC	2010 TCAAAGCACT TCAAAGCACT	2100 ACCITAAAGA ACCITAAAGA
SEQ ID NO 11(1912) 1912 SEQ ID NO 11(1912) TGCT SEQ ID NO 4(1762) TGCT SEQ ID NO 13 (306) SEQ ID NO 16 (1) SEQ ID NO 15 (1) SEQ ID NO 17 (1) Consensus(1912)	SEQ ID NO 11(2003) 2003 2010 2020 2030 2040 SEQ ID NO 11(2003) CCATTCAAAGCACTATGCTAAGTCCTTTATGTGAATTAACTT SEQ ID NO 13 (306)	SEQ ID NO 11(2094) 2094 SEQ ID NO 11(2094) TCCT SEQ ID NO 4(1944) TCCT SEQ ID NO 13 (306) SEQ ID NO 16 (1) SEQ ID NO 15 (1) SEQ ID NO 17 (1) Consensus(2094)

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(2185)	(2185) 2185 2190	2200	2210	2220	2230	2240	2250		Section 25 2275
SEQ ID NO 11(2185) AGTCTAACTCCAGGTATAATAACATT SEQ ID NO 4(2035) AGTCTAACTCCAGGTATAATAACATT SEQ ID NO 13 (306)	88) AGTCTAACTC 33) AGTCTAACTC 806) (1) (1) (1)	CAGGTATAATAA CAGGTATAATAA 	CATTATGCTAC CATTATGCTAC	ATGCTACTGTTTGCAGCTT ATGCTACTGTTTGCAGCTT	TTGACTATG(CCTGAATTATA CCTGAATTATA 	ACGTCATGCT ACGTCATGCT 	ATGCTACTGTTTGCAGCTTTGACTATGCCTGAATTATAACGTCATGCTATCTAACTAA	CTTAA
(2276)	(2276) 2276	2290	2300	2310	2320	2330	2340	2350	2366 2366
SEQ ID NO 11(2276) GGGAAATA SEQ ID NO 4(2126) GGGAAATA SEQ ID NO 13 (306) SEQ ID NO 16 (1) SEQ ID NO 15 (1) SEQ ID NO 17 (1) Consensus(2276)	76) GGGAAATAAA 26) GGGAAATAAA 36)	AAATGAGCCATAG AAATGAGCCATAG 	GGCTCAATTTC GGCTCAATTTC 	ATAAAAGGAGA ATAAAAGGAGA 	GAAAATACT(GAAAATACT(GAAAATACT(3GGGAAAAGTG 3GGGAAAAGTG 	ATAATGCAGAATAAATGCAGA	AAAATATIT AAAATATIT	TTGTA
(FOCO)		0000	0000	000	0				Section 27
SEQ ID NO 11(2367) AAAG SEQ ID NO 4(2217) AAAG SEQ ID NO 13 (306) SEQ ID NO 16 (1)	(2367) 2356/ (2367) AAAGTGCCAG (2217) AAAGTGCCAG (306)	AGATTGAGTAT AGATTGAGTAT 	AACAAGIGIGA AACAAGIGIGA 	Z4UU CCAAAAAAAA CCAAAAAAAAAA 	2410 1AAAAAAAAA 1AAAAAAAAA 1	2420 14848466846 1484866846 1	2430 3AAGGTAAAAA 3AAGGTAAAAA 	SEQ ID NO 11(2367) 2350 2450 2450 2450 2450 2450 2450 2450 24	745/ [GAGA [GAGA
236	(1)								

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SEQ ID NO 11(2458) AATAGAAATATCAGAGGAAGTAAATAAAGGAGGTGAGAGTTAAATTCTCTTTTAGCATTCCACAGATTCCACAGATTCCACAATCACATTTCT SEQ ID NO 4(2308) AATAGAAATATCAGAGGAAATAAAGGAGGGTGAGGTAAATTCTCTTTTAGCATTCCACAGATTCCACAAATCACATTTCT SEQ ID NO 13 (306)	TCAGAGGAAG TCAGAGGAAG	GAAATAAAG GAAATAAAG 	3AGGGTGAGA 3AGGGTGAGA 1	STAAATTCTC STAAATTCTC	TITIAGCAT TITITAGCAT TITITAGCAT TO T	TCAGATTCCA TCAGATTCCA 	CAGATTCCACAAA CAGATTCCACAAA	AATCACATTTCT AATCACATTTCT
Consensus(2458) (2549) 2549 EQ ID NO 11(2549) TITITIACCA? SEQ ID NO 4(2399) TITITIACCA? EQ ID NO 13 (306)	2560 ACTAAGGAAA ACTAAGGAAA	2570 AATAACACT AATAACACT	2580 IGACCTAACA	2590 FITCATIGCA	2600 GITAGCIAAA	2610 AGGATGCTAG	2620 AAAACTATGTTG AAAACTATGTTG	Section Section CAGTGGTT CAGTGGTT
EQ ID NO 11(2549) TITITIACCA! SEQ ID NO 4(2399) TITITIACCA! EQ ID NO 13 (306)	ACTAAGGAAA ACTAAGGAAA	AATAACACT AATAACACT 	GACCTAACA'	TITCATIGCA TITCATIGCA	GTTAGCTAAAAGTTAAAAAAAAAAAAAAAAAAAAAAAAA	AGGATGCTAG AGGATGCTAG	AAAAACTATGTTG AAAAACTATGTTG	CAGIGGII CAGIGGII
SEQ ID NO 15 (1) SEQ ID NO 17 (1)								
		00000	0200	0000	0000	0020		Sectic
TAATTIC TAATTIC	Z650 TTCAGGAATA TTCAGGAATA	Z660 GAGAAAAGT GAGAAAAGT	ZB/O SACAAAAAGA' SACAAAAAGA'	Z680 CCAGAGAAGA CCAGAGAGAGA	2690 GAAGAAAGG GAAGAAAGG	AAACTATCAG AAACTATCAG	Z/10 AAAAATACAGAAT AAAAATACAGAAT	2720 2730 TTGGAGTAGGA TTGGAGTAGGA
SEQ ID NO 16 (1)								

align SEQID#4 against SEQID#11.apr

2760 2800 2821 2821 2821 2821 2800 2821 2800 2821 2801 280	2900 2912	SEQ ID NO 11(2822) TCTGCCGAGGGCTTGTTAAAAAGGCAGAATCTCAGGTCCCATCCCAGACTCACTGAATCAGAATATAAATACTGACAAAGATGCCCCGGGAT SEQ ID NO 4(2672) TCTGCCGAGGCCTTGTTAAAAAGGCAGAATCTCAGGTCCCATCCCAGACTCACTGAATCAGAATACTGACAAGATGCCCCGGGAT SEQ ID NO 13 (306)	2990 3003	1.GGAAGAA
2800 TIGGICCCIGG/ TIGGICCCCIGG/ TIGGICCCCIGG/ TIGGICCCCIGG/ TIGGICCCCIGG/ TIGGICCCCIGG/ TIGGICCCCIGG/ TIGGICCCCIGG/ TIGGICCCCIGG/ TIGGICCCCIGG/ TIGGICCCCIGG/ TIGGICCCCIGG/ TIGGICCCCIGG/ TIGGICCCCIGG/ TIGGICCCCIGG/ TIGGICCCCCIGG/ TIGGICCCCCIGG/ TIGGICCCCCIGG/ TIGGICCCCCIGG/ TIGGICCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	2890	ATAATACTGA(ATAATACTGA(2980	TTCTGAGTTTTTTCTGAGTTTTTTTTTTTTTTTTTTTTT
2790 SCTACTICAGTI SCTACTICAGTI	2880	GAATCAGAAT/	2970	CAACTTAGTAT
2780 TAAGTATCTTG TAAGTATCTTG	2870	CCAGACTCACT	2960	ATTGTTTTCTG ATTGTTTTCTG ATTGTTTTCTG
2770 ATTGTAATCT ATTGTAATCT	2860	AGGICCCATC.	2950	GTAGCCTGTGGGGTAGGCCTGTGTGGTGGTGTGTGTGTGT
2760 FAAATTTTAT FAAATTTTAT 	2850	96CAGAATCTC 96CAGAATCTC 1	2940	AAGTICCATT
2750 GGGTTGAAGGT GGGTTGAAGGT	2840	TTGTTAAAAA(TTGTTAAAAA(CTTAAAAA(CTTAAAAA(CTTAAAAAA(CTTAAAAAAAA	2930	TAGAGCTGGCC
14 2740 TAACATATIT TAACATATIT 	2830	TGCCGAGGCC TGCCGAGGCC TGCCGAGGCC	3 2920	ATATGCACAG
SEQ ID NO 11(2731) 2731 2740 2750 2760 SEQ ID NO 11(2731) TATAACATATITGGGTTGAAGGTAAAATTTTATAT SEQ ID NO 4(2581) TATAACATATITGGGTTGAAGGTAAAATTTTTATAT SEQ ID NO 13 (306)	(2822) 2822	SEQ ID NO 11(2822) TCTGCCGA SEQ ID NO 4(2672) TCTGCCGA SEQ ID NO 13 (306) SEQ ID NO 16 (1) SEQ ID NO 15 (1) Consensus(2822)	(2913) 2913	SEQ ID NO 11(2913) TCA SEQ ID NO 4(2763) TCA SEQ ID NO 13 (306) SEQ ID NO 16 (1) SEQ ID NO 15 (1) SEQ ID NO 17 (1) Consensus(2913)

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Section 34 3094	GTGCCTGAG GTGCCTGAG 	3185	CATICCICIATITA CALICCICIATITA	3276	GGAGACIAACICI GGAGACIAACICI
3080	TCTCCTTTACTTACTAGCTGCATGACTCATGAGCAAGGAAATCAAACTTTATGTGCCTGAG TCTCCTTTACTTACTAGCTGCATGACTCATGAGCAAGGAAATCAAACTTTATGTGCCTGAG	3170	TGAGGATGTTCAACAAAIGCTCCTTTCAITCCTCTAITTA TGAGGATGTTCAACAAAIGCTCCTTTCAITCCTCTAITTA	3260	AGCAGCCTTIGIGCTALTAICIGITITICIAAACTIAGTAATIGAGIGTGATCTGGAGACTAACTCT AGCAGCCTTIGIGCTATTATCTGTTTTCTAAACTIAGTAATIGAGIGTGATCTGGAGACTAACTCT
3070	AGCAAGGAAAT AGCAAGGAAAT 	3160	ATGITCAACAAAIGCI AIGITCAACAAAIGCI 	3250	TCTAAACTTAGTAAITGAGTGTGATCT TCTAAACTTAGTAAITGAGTGTGATCT
3060	ATGACTCATGATGACTCATGA	3150	1GAGGAZGZTC 1GAGGAZGZTC 1G	3240	CTAAACTTAC
3050	TACTAGCTGC/	3140	AGGCTTGTTTT AGGCTTGTTTTTTTTTTTTTTTTTTTTT	3230	TTATCTGTTT TTATCTGTTT TTATCTGTTT TTATCTGTTT TTATCTGTTT
3040	CTCCTTTTACCTTTTACCTTTTTTTTTTTTTTTTTTTT	3130	ATAATAATCATCTCCTAGGCTTGTT ATAATAATCATCTCCTAGGCTTGTT	3220	AGCAGCCTTTGTGCTATTATCTGT AGCAGCCTTTGTGCTATTATCTGT
3030	GTGTT GTGTT GTGTT GTGTT	3120	3ACTATAATAA 3ACTATAATAA 	3210	FGCTAGCAGC
3020	CTTCTGGCAGACTTCTGGCAGACTTCTGGCAGACTTCTGGCAGACTTCTGGCAGACTTCTGGCAGACTTCTGGCAGACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT	3110	ATAAAATGGA(ATAAAATGGA(3200	CAGACAATTC CAGACAATTC
3010	AGGCCTTAGC	3100	CCTCATCT	(0)	AACCTGCCGCGCGCGCGCGCGCGCGCGCGCGCGCGGCGGCGG
(3004) 3004	SEQ ID NO 11(3004) CCAGGCCTTAGCTTCTGGCAGACTT SEQ ID NO 4(2854) CCAGGCCTTAGCTTCTGGCAGACTT SEQ ID NO 13 (306)	(3095) 3095 3100	SEQ ID NO 4(2945) TITCCICATCTATAAAATGGAGACTATAATAATCATCTCCTAGGCTTGTTTTGAGGATGATCAAAATGCTCCTTTCATTCCTCTAATTAA SEQ ID NO 4(2945) TITCCTCATCTATAAAATGGAGACTATAATAATCATCTCCCTAGGCTTTTGAGGATGATCAAAAAAAA	(3186) 3186	SEQ ID NO 11(3186) CAGACCTGCCGCAGACAATTCTGCT SEQ ID NO 4(3036) CAGACCTGCGGCGGCAGCAATTCTGCT SEQ ID NO 13 (306)

	(3277) 3277	3290	3300	3310	3320	3330	3340	3350	3367
SEQ ID NO 11(3277) GAAATAAATAAGCTGATTATTTAATTTA SEQ ID NO 4(3127) GAAATAAATAAGCTGATTATTTATTTA SEQ ID NO 13 (306)	AAATAATA AAATAATA 	AGCIGATIA AGCIGATIA 	TITATITATI TITATITATI 	FICTCAAAACA FICTCAAAACA 	AACAGAATAC 	GATTIAGCAA GATITAGCAA 	ATTACLICI ATTACTICI 	GATATTAT GATATTAT 	CATTICTA
SEQ ID NO 15 (1)	(1) (1)	 AGCTGATTA AGCTGATTA	TTATTATT TTATTATT	TCTCAAACE	AACAGAATAC	GATTTAGCAA	ATTACITCI	SEQ ID NO 16 (1)	
(3368) 3368	68	3380	3380	3400	3410	3420	3430	3440	3458
SEQ ID NO 11(3368) TATTOT SEQ ID NO 4(3218) TATTOT SEQ ID NO 13 (306) SEQ ID NO 16 (1) SEQ ID NO 15 (1)	ATTCTCCTA ATTCTCCTA ATTCTCCTA	CCCTGAGTTC	GATGTGTGAGG	CAATATGTCAA	TTTCATAAA	AGCCAGGTATA AGCCAGGTATA 	CATTATGGA(CATTATGGA(SEQ ID NO 11(3368) TATTCICCIACCCIGAGITGATGIGIGIGGGAATAIGICACITICATAAGGCCAGGIAIGATTAIGGACAGGIAAGIAAAAAACAIAITAT SEQ ID NO 4(3218) TATTCICCIACCCIGAGITGIGIGIGGGCAATAIGICACITICATAAAGCCAGGIAITAIGGACAGGIAAGIAAAAAAAAAA	CCATATATATATATATATATATATATATATATATATATA
SEQ ID NO 17 (218) TATICICCTACCCIGAGITGAIGIG Consensus(3368) TATICICCTACCCIGAGIIGAIGIG	TICICCIA ATICICCIA	CCCTGAGTIC	GATGTGTGAGG	CAATAIGICA(CAATAIGICA(TITCATAAA SITICATAAA	GCCAGGTATA	CATTATGGA CATTATGGA(SEQ ID NO 17 (218) TATTCICCIACCCIGAGITGAIGIGIGAGCAATAIGICACITICATAAAGCCAGGIAIACATTAIGGACAGGIAAGTAAAAAAAATAITAT Consensus(3368) TATTCICCIACCCIGAGITGAIGIGIGAGCAAIAIGICACITICAIAAAAGCCAGGIAIACAITAIGGACAGGIAAGIAAAAAAAAAA	CATATIAT CATATIAT — Section 39
(3459) 3459	59	3470	3480	3490	3500	3510	3520	3530	3549
SEQ ID NO 11(3459) TTAT SEQ ID NO 4(3309) TTAT SEQ ID NO 13 (306) SEQ ID NO 16 (1)	459) TRAITCIACG 309) TRAITCIACG 306)	TTTTGTCC	AAAATTTTAA AAAATTTTAA 	AATTTCAACTC	STIGCGCGIG	TGTTGGTAAT TGTTGGTAAT	GTAAAACAAA GTAAAACAAA	SEQ ID NO 11(3459) TTATTCTACGTTTTTGAAATTTTGAACTGTTCGCGGTGTGGTGGTAATGTAAACAAAC	ATTCAGT ATTCAGT
SEQ ID NO 15 (1)SEQ ID NO 17 (309) TRATICIACGITITIGICCRARARI Consensus(3459) ITATICIACGITITIGICCARARATI	 RATICIACE RATICIACG	TTTTGTCC	 &&&&ATITIA &&&ATTTTA			TGTTGGTAA-TGTTGGTAA-			

align SEQID#4 against SEQID#11.apr

(3550) 3550	3560	3570	3580	3590	3600	3610	3620	3630	3640
SEQ ID NO 11(3550) CAGTATITIAAGCCCCTGTACTIAAACATATICCTCGTACCAATGAAAGGTAAAAAGCAAATTIGTGTGAGATATCGTAGAAGTA SEQ ID NO 4(3400) CAGTATITAAGCCCCTGTACTTAAACATATICCTCGTACCATGAAGTTACCATGAAAAGCAAATTTGTGTGAGATATCGTAGAAGTA SEQ ID NO 13 (306)	ATITAAGCCCCT AITTAAGCCCCT	GTACTTAAACA GTACTTAAACA 	ATATICCTCGTACCAAIGAAGTTACAIGAAAAGCAAATTTGTGTGAGATATCGTAGATGGAAGTA ATATICCTCGTACCAATGAAGTTACATGAAAAGCAAATTTGTGTGAGATATCGTAGATGGAAGTA 	CCAATGAAG; CCCAATGAAG; 	ITACATGAAA ITACATGAAA 	AGCAAAIIIG AGCAAAIIIG 	TGTGAGATATC TGTGAGATATC	GTAGATGG1 GTAGATGG1 	AGTA
SEQ ID NO 17 (367) Consensus(3550)								S S S S S S S S S S S S S S S S S S S	Section 41
(3641) 3641	3650	3660	3670	3680	3690	3700	3710	3720	3731
SEQ ID NO 11(3641) AATTAGTCTTTATGTTCCCCACAAATTGAAATGCATTTCAAAAACTCTGTGTGTG	AGICITTATGIT AGICITTATGIT 	CCCCACAAATT	TGAAATGCATTTCAAAAACTCTGTGTGTGTATGTGTGTGT	CAAAAACIC	[GTGTGTA]	1 G 1 G 1 G 1 G 1 G 1 G 1 G 1 G 1 G 1 G	TGTGTGTGTGTCACAGAGTGTGTGTGAGAGAGAGAGTGTGTGT	GTGTGAGA(GTGTGAGA(GTGTGAGA(GTGTGAGA(GTGTGAGA(GTGTGAGA(GTGTGAGA)))	A G A A B A B A B A B A B A B A B A B A
			4		4		4 4		Section 42
(3732) 3732 3740 3810 3822 SEQ ID NO 11(3732) A CAGAGAGATACGATTAGATTAATAAGACCAAGTTTTCTAAAAAATGAGATCATAACAAAAGC SEQ ID NO 11(3732) ACAGAGATACGCTTTGGTTGCCTCCATAAGCTGGCTGCTATGATTAATAAGACCAAGTTTTCTAAAAAAATGAGATCATAACAAAAGC SEQ ID NO 4(3582) ACAGAGAGATACGCTTTGGTTGCCTCCATAAGCTGGCTGCTATGATTAATAAGACCAAGTTTTCTAAAGAAAATGAGATCATAACAAAAGC	3740 AGAGATACGCTT AGAGATACGCTT	3750 TGGTTGCCTCC	3760 3800 3870 3822 SE22 CATAAGACTAAAGACAAAATAAGACAAAAGTTTTCTAAAAAAAA	3770 GCTATGATT	3780 AATAAGACCA	3790 AGTTTTCTAA AGTTTTCTAA	3800 AGAAAATGAGA AGAAAATGAGA	3810 TCATAACAA	3822 AAGC AAGC
SEQ ID NO 13 (306)))
ID NO 15 (1)									
SECTIONO 17 (367): Consensus(3732)		 	 	 		 	 		

SECID NOV (1982) SECID NOV (1	TCTTTATGACTATCTTTTATCAGGGGCA TCTTTATGACTATCTTTTATCAGGGGCCA	aaaaggaaagaga aaaaggaaagag	CAAAACAGCAT CAAAACAGCAT	2 C 20 C 20 C 2 C 2 C 2 C 2 C 2 C 2 C 2		ദകവ	3913
GGGCAAAAGGAAAACGACAAAACAGCATGAAATGATGAGGACCAAGTGATGAAATTCATTC				GAAATGATGA GAAATGATGA 	GACCAAGTG/ GACCAAGTG/ 	ATGAAAATTCA ATGAAAATTCA 	FICACAA FFCACAA
GGGCAAAAGGAAAACAGCATGAATGATGAGACCAAGTGATGATGATAATTCATTC							 :ICACAA
0 3930 3960 3960 3980 3990 TICAAGAGIAATICTOTIGGGTAATICAGCAGCCTGTTACTATGGCTCTCTGGAGTGATAGCTAATGTAATGAAGCCTTTCAAGAGTATTCTCTTGGGTAATTCTATGCTAATGAAGCCTTTACTATGGCTCTTTGGGAGTGATAGCTAATGTAATGAAGCCTTTCAAGAGTAATTCTCTTGGGTAATTCTATGGTAATGAAGCCTTTCAAGAGTAATTCTCTTGGGTAATTCAAATGAAGCCTTTAATGCAAGAGTAATAGTAATGAAGCCTTTAATGCTAATGGTAATGAAGCCTTTCAAGAGTAATAGTAATGAAGAATAAAAATTCTCTTGGGTAATTCAAGAATAATGCAACAGAAATAAAAAAAA	ATTGCTTTCAAGAGTAATTTCTCTTGG(CAAAACAGCAI		GACCAAGIGA	ATGAAAATTCA	 FTCACAA Section 44
TICAAGAGTAATITCTCITGGGTAATTCAGCAGCCTGTTACTATGGCTCTCTGGAGTGATAGCTAATGTAAATGAAGCCT TICAAGAGTAATTTCTCTTGGGTAATTCAGCAGCCTGTTACTATGGCTCTCTGGAGTGATAGCTAATGTAAATGAAGCCT Section 4020 4030 4040 4050 4060 4070 4080 TTATCCTGACAAGAATATACTCAGCCAATAATGCAACAGAAATCCATTCAAAGCATTCGGGAAAAATTCAAAGAATAAA TTATCCTGACAAGAATATACTCAGCCAATAATGCAACAGAAATCCATTCAAAGCATTCGGGAAAAATTCAAAAGAATAAA	ALGCIICAAGAGIAAIIICICIIGGG	3950 GTAATTCAGCAGCC	3960 TGTTACIATGO	3970 SCICICIGGAG	3980 IGATAGCTAJ	3990 ATGTAAATGAAA	4004 3CCICIR 3CCICIR
TICAAGAGIAATITCICITGGGTAATICAGCAGCCIGITACIAIGGCTCICTGGAGIGAIAGCIAATGIAAATGAAGCCI Sedio 4020 4030 4040 4050 4060 4070 4080 TTAICCTGACAAGAATATACTCAGCCAATAATGCAACAGAAATCCATTCAAAGCATTCGGGAAAAATTCAAAGAATAAA TTAICCTGACAAGAATATACTCAGCCAATAATGCAACAGAAATCCATTCAAAGCATTCGGGAAAAATTCAAAAGAATAAA TTAICCTGACAAGAATATACTCAGCCAATAATGCAACAGAAATCCATTCAAAGCATTCGGGAAAAATTCAAAAGAATAAA	ATTGCTTTCAAGAGTAATTTCTCTTGGC	GIAATICAGCAGCC	 TGTTACIAIG	CICICIGGAG	TGATAGCEA		
4020 4030 4030 4040 4050 4060 4070 4080 ITATCCTGACAAGAATATACTCAGCCAATAATGCAACAGAATCCATTCAAAGCATTCGGGAAAAATTCAAAAGAATAAA TTATCCTGACAAGAATATACTCAGCCCAATAATGCAACAGAATCCATTCAAAGCATTCGGGAAAAATTCAAAAGAATAAA TTATCCTGACAAGAATATACTCAGCCAATAATGCAACAAATCCATTCAAAGCATTCGGGAAAATTCAAAAGAATAAA	GCTTTCAAGAGTAATTTCTCT	GTAATICAGCAGCC	TGTTACTATGO	CTCTCTGGAG	TGATAGCTA	ATGTAAATGAA(SCCTCTA Section 45
AAAGIGGAITAICCIGACAAGAATATACICAGCCAATAATGCAACAGAATICCATICAAAGCATICGGGAAAAATTCAAAAGAATAAATATAAATAATATAAATAA	4020	4040	4050	4060	4070	4080	4095
1-4	AGTGGATTATCCTGACAAGAATATACTC AGTGGATTATCCTGACAAGAATATACTC	CAGCCANTAATGCA CAGCCAATAATGCA	ACAGAAA I IOO ACAGAAA I IOO	ATTCAAAGCAT ATTCAAAGCAT 	TCGGGAAAA/ TCGGGAAAA/ 	ATTCAAAAGAA ATTCAAAAGAA 	CABATAT CABATAT
	1 3-4	CAGCCAATAATGCA	 acagaaatco	 ltcaaagcat	TCGGGAAAA.	 hitcarargar	 Frames

(4096) 4096	4110	4120	4130	4140	4150	4160	4170	Section 46 4186
	ntititititaaag Kititititaaag	TTAATGACCTA TTAATGACCTA 	OGATCCATT	COTTCCCTGAC	TAACAAGCA(TAACAAGCA(SCAAGCACTT SCAAGCACTT 	AAAAATATCCAG AAAAATATCCAG 	CCAGGATGAA CCAGGATGAA
SEQ ID NO 16 (1)	TITITITITIAAAG	TAATGACCTA		19-1	CTAACAAGCA(GCAAGCACTT		 CCASGATGAA
Consensus(4096) ICTITITITITITAAAGTIAAIG.	TITITITITAAAG	TAAIGACCIA	ACGATCCATT	CTTCCCTGAC	TAACAAGCAG	SCAAGCACTT	acctacgatccatttcttccctgactaaccagcaagcacttaaaaatatccagccag	CCAGGATGAA Section 47
(4187) 4187	4200	4210	4220	4230	4240	4250	4260	4277
SEQ ID NO 11(4187) ATAGAAACCCACCTGACTTGTTAATATTTTTGTTTGGTCCCAGGGACTCGAGGATTCTAAGCCAAATTCTTTGAATGATCTTGGCAAATGTCT SEQ ID NO 4(4037) ATAGAAACCCACCTGACTTGTTAATATTTTTGTTTGGTCCCAGGGACTCAAGATTCTAAGGCCAAATTCTTGAATGATCTTGGCAAATGTCT SEO ID NO 49 / 2008)	AAACCCACCTGACTT	STIAAIATITI STIAAIAITI	TGTTIGGTC	CAGGGACTC/	NGATICIAAG NGATICIAAG	CCAAATTCTT	TGAATGATCTTS TGAATGATCTTC	GCAAATGTCT GCAAATGTCT
SEQ ID NO 16 (1)	AAACCCACCTGACTT	3TTAATATIT	TGTTTGGTC			 30AAATTOTT	TITITGITIGGICCCAGGGACTCAGATICIAAGCCAAATICITGAATGATCTTGGCAAATGTCT	CAAATGICI
SECTIONO 17 (387) ATAGAAACCCACCTGACTTGTTAAT Consensus(4187) ATAGAAACCCACCTGACTTGTTAAT	AAACCCACCIGACII		TGTTTGGTC	CAGGGACICA	GATTCTAAG	CCAAATTCTT	TIGGICCCAGGGACICAGAITCIAAGCCAAAIICITIGAAIGAICITIGGCAAAIGICI Section 48	GCAAATGTCT Section 48
(4278) 4278	4290	4300	4310	4320	4330	4340	4350	4368
+ + -	TTATTTTGCCAACT TTATTTTGCCAACT	TITCITIATO TICITIATO	TGGAAAAAA TGGAAAAAAA	AGITICATGAZ AGITICATGAZ 	ATGGGTGTCA ATGGGTGTCA	AAATTGATTA AAATTGATTA 	GIIITAAAAACC GIIITAAAAACC	TITCIIGCAG
SEQ ID NO 10 (1)	TRATITICCCAACT		.TGGAAAAA?	GTTTCATGA	TGGGTGTCA	 saattgatta	 SITIAAAAACO	TTTCTTGCAG
SEC ID NO 17 (307)	 TTATTTTGCCAACT	I ⊟	 TGGAAAAAA		ATGGGTGTCA	 AAATIGATIA	 Taictiggaaaaaagiticaigaaigggigicaaaaaiigaiiagititaaaaacciiiceigcag	TITCIIGCAG

(4369) 4369	369	4380	4390	4400	4410	4420	4430	4440	Š	Section 49 4459
SEQ ID NO 11(4369) ATACGTATGGCACCCTAAAACTGTATTAGAAAAAGTAAGT	VEACGEA.	RGGCACCCTA RGGCACCCTA 	AAACTGTATTA AAACTGTATTA	TTAGAAAAAAGT. TTAGAAAAAA—— 	AAGTACTCT	GTAGTGTGA? 	AAATTCTTAA 	AGGACACCCI 	CTTTTACAA 	ACTCA
SEQ ID NO 16 (1)SEQ ID NO 15 (522) ATACGTATESCACCCTAAAACTGTA	TACGIAS		1 35-4	 Tagaaaaaaa						
SEC ID NO 17 (36/)	TACGTA	IGGCACCCIA	 .AAACTGTATTA	 TTAGAAAAAAA	 	 		! ! ! ! !	<i>d</i>	Soction 50
(4460) 4460	460	4470	4480	4490	4500	4510	4520	4530	4540	4550
SEQ ID NO 13 (306)										Section 51
(4551) 4551	551	4560	4570	4580	4590	4600	4610	4620	4630	4641
SEQ ID NO 11(4551) IGGCAGGIGIGGIGGCICACCCIGIAAITCCAGCACITIGGGAGGCCAAGGCGGGCGGATCACCIGAGAICAGGAGITCAGGACCAGCCI SEQ ID NO 4(4255)	.GGCAGG	IGTGGTGGCT	CACACCIGIAA	TTCCAGCACT	TTGGGAGGC	CAAGGCGGG(CGGATCACCTG	AGATCAGGAG	TTCAGGACC	AGCCT
SEQ ID NO 17 (367) Consensus(4551)										

align SEQID#4 against SEQID#11.apr

4730 4710 4720 4732 4732 4732 4732 4732	1	4780 4790 4800 4810 4823	SEQ ID NO 414733) TGAGGCAGGAGAATCACTTGAACTCAGGAGTTGCAGTGAAGTCATGCCACTGCACTCCAGCCTGGGTGACAAGA SEQ ID NO 44255)	4870 4880 4890 4900 4914
4680	ACAAAAATCACCC	7270	GGTTGCAGTGAGC	4860 48
4670	TTTACTGAAAAT	4760	CTCAGGAGTCAGA(4850
4660	AAACCCAGTC:	4750	TCACTTGAACT	4840
4650	AATATGGTG	4740	3CAGGAGAA	4830
(4642) 4642	SEQ ID NO 11(4642) GATCAATATGGTGAAACCCCAGTCTT SEQ ID NO 4(4255)	(4733) 4733	SEQ ID NO 11(4733) TGAGGCAG SEQ ID NO 4(4255) SEQ ID NO 13 (306) SEQ ID NO 16 (1) SEQ ID NO 15 (558) SEQ ID NO 17 (367) Consensus(4733)	(4824) 4824

align SEQID#4 against SEQID#11.apr

(4915) 4915 4920	4930	4940	4950	4960	4970	4980	4990	5005
SEQ ID NO 41(4915) CCTAGITIGGGTAATGGCCCTCTGGGCAGGACTGGAGTGGGGCCACACGGAGAAGCTGCAAACTATGTTTAGAAGCATGTCTGGGAAATGT SEQ ID NO 4(4255)	GGTAATGGCCC	TCTGGGCAGG7	ACIGGAGIGG(3GCACACAGA 1	GAAGCTGCAA	AACTATGTTT	AGAAGCATGTCTG	GGAAATGT GGAAATGT GOOGLOOT
(5006) 5006	5020	5030	5040	5050	5060	5070	5080	5096
SEQ ID NO 13 (306) SEQ ID NO 16 (1) SEQ ID NO 15 (558) SEQ ID NO 17 (367) Consensus(5006)								
(5097) 5097	5110	5120	5130	5140	5150	5160	5170	— Section 5787
SEQ ID NO 11(5097) GAGAAGCAAAAGTGGGGAAGCAAGAGGAATTATGCTTT SEQ ID NO 4(4255)	AAGTGGGGAAG(CAAGAGGAAT7	TATGCTTTTC.	TCATCAGCCAAAT		GAGGATTGG	CICAGICAICIIG	CTTGGCTGAGGC
SEQ ID NO 15 (558) SEQ ID NO 17 (367) Concensis(5097)								

align SEQID#4 against SEQID#11.apr

(5188) 5188	5200	5210	5220	5230	5240	5250	5260	Section 58 5278
SEQ ID NO 11(5188) TCATGAAACCCAGGTGAAAGCTAGATTACATTACAGGAAGGA	TGAAACCAGGTGT/ 	AAAGAAAGTGGA 	CTAGATTAATT	TCATCCATT	ACAGGAAGAG 	3AGCCGTGAA/ 	AGATAATCCAGA/A/A/A/A/A/A/A/A/A/A/A/A/A/A/A/A/A/	AATCATTGGGA
SEQ ID NO 17 (367) Consensus(5188)								Section 59
(5279) 5279	5290	5300	5310	5320	5330	5340	5350	5369
SEQ ID NO 4(4255)	7	I <th>\$\ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \</th> <th>5 </th> <th>+ </th> <th>- </th> <th> </th> <th></th>	\$\ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \	5	+	-		
								Section 60
(5370) 5370	5380	5390	5400	5410	5420	5430	5440	5450 5460
SEQ ID NO 11(5370) TACCCATGAGTTGACTCAGAAAAACATAAAAAGTATTGTTGCTCTGGTCAGAGTTTTATCTAACTCATTCTCACTTCTTATTCCATGATG SEQ ID NO 44(4255)	CCATGAGTTGACT(CAGAAAAAACAT 	AAAAAGTATTG 	TTGCTCTGC	TCAGAGTTTT.	ATCTAACTCA:	TTCTCACTTCTT/	ATTCCATGATG
SEQ ID NO 16 (1)								
SEQ ID NO 17 (367)								
Consensus (5370)								

align SEQID#4 against SEQID#11.apr

(5461) 5461	5461	5470	5480	5490	5500	5510	5520	5530	5540	Section 615551
SEQ ID NO 11(5461) AAATGACATAAATGAGGTTTTTTAT SEQ ID NO 4(4255)	AAATGA(ACATAAATG.	AGGTTTTTTAT	TGTTGTTGTTGTTGTTTGTTTGTTTGTTTGTTTGTTTG	1GTTGTTGTTGTTTTTCTGGACACAAGGCAAGGTAGCTACCTGGGCAGAGCTGTTTTATTTCTC	GGACACAGG	SCAAGGTAGC	TACCTGGGCCA	GAGCTGTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	A
(5552) 5552	5552	5560	5570	5580	5590	5600	5610	5620	5630	Section 625642
SEQ ID NO 11(5552) TATGCCGTGGAGAAATTGGTTAAT SEQ ID NO 4(4255)	TATGC	CGTGGAGAGAAA	AAATTGGTTAA	TTGGCCATGG	IGGCCAIGGAAGGCAGICATIAAGAIGIICCCAIGCGAGIGAACIITCCAGGGIICCCAGCCIICI	TTAAGATGT	CCCATGCGA	GIGAACTITIC	CAGGGTTCC 	AGCTTCT
(5643) 5643	5643	5650	5660	5670	5680	5690	5700	5710	5720	Section 635733
SEQ ID NO 11(5643) GCATCCTTCCCTGTCCCTCAATTCCA SEQ ID NO 44(255)	GCATCC GCATCC 	THE COLIE	TCCCTCAATTCC	ATTGTTGGTG	TIGITGGTGATGACAATGTCTCCCCATCAGCCTCATGAAGTTCTCTCTC	CTCTCCCAT(CAGCCTCATG,	AAGITCTCTC	TCATITATT/	AAATTTG

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align SEQID#4 against SEQID#11.apr

SEQ ID NO 11(5734) CTTTCAGGAAAATTTTGAAAATGT SEQ ID NO 4(4255)	AATTTTGAAAA	TGTGTCCAGTF	GTCCAGTAATGCCTGATTGGCCCCTTATCCTAAAGGCTTAAACTGGAGGAAGGA	TGGCCCCTIA	TCCTAAAGGC	TTAAACTGGA	A L J B A B B B A B B	ر د د د د
(5825) 5825 5830 SEQ ID NO 11(5825) AAA TCTTGCAAA SEQ ID NO 4(4255) SEQ ID NO 13 (306) SEQ ID NO 16 (1)								
SEQ ID NO 11(5825) AAATCTTGCAAA SEQ ID NO 4(4255) SEQ ID NO 13 (306) SEQ ID NO 16 (1)	5840	5850	5860	5870	5880	2890	5900	- Section 65 5915
SEQ ID NO 4(4239)	ATCATIGAGCC	AACGTAT	TAATAGCAAGATCTATCAT	ATCTATCATT	TATIGACTAG	TATGTGGCAG	CCCTIT	TATT
SEO ID NO 16 (1)								
SEO ID NO 15 (558)								
SEQ ID NO 17 (367)								
Consensus(5825)								Section 66
(5916) 5916	5930	5940	5950	5960	5970	5980	5990	9009
SEQ ID NO 11(5916) GCAGGGAGAGTIGATGGGGGGGGGGGGGGGGTTCACATCTTAAAGAGGTGCTATCTCCTCTATATAAATCATGTAAGTCAAGAGTAAGG	IGATGGGGGGG	GCGGGGTTCAC	CACATCTTAA	AGAGGIGCIA	TCTCCTCCTA	TATAAATCAT	GTAAGTCAAGAG	AGTAAGG
SEQ ID NO 13 (306)								
SEQ ID NO 16 (1)								
SEQ ID NO 15 (558)								
SECTION 17 (307) ====================================	 	 	 	 	 	 	 	

align SEQID#4 against SEQID#11.apr

2009 (2009)	8020	6030	6040	8050	9080	6070	9080	Section 67
SEQ ID NO 11(6007) AATTGTTTTGTTTTGGTTATATTCAGGGGATTAGAGTATACAGTAGAAGATCCCAAGAAACCTTGGGATCATTTTAGACTAAGAAATGCCA SEQ ID NO 4(4255)	GTCTTTGTTTGGTT.	ATATICAGGGG/ 	ATTAGAGTAT.	ACAGTAGAAGA	ATCCCAAGAA.	ACCTTGGGAT	CATITIAGACTAAGA)	AATGCCA
SEQ ID NO 15 (558) SEQ ID NO 17 (367) Consensus(6007)								Section 68
8609 (8609)	6110	6120	6130	6140	6150	6160	6170	6188
SEQ ID NO 11(6098) ATACCGCCGGGCGCGGTGGCTCACGCCTGTAATCCCAGCACTTTGAGAGGCCGAGGTGGGCGGATCACAAGGTCAGGAGATTGAGACCGTC SEQ ID NO 13 (306)	0	SCTCACCTG	TAATCCCAGC	ACTITGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	CCCAACCAACCAACCAACCAACCAACCAACCAACCAAC	3CGGATCACACACACACACACACACACACACACACACACAC	AGGTCAGGAGATTGA(A C C C C C C C C C C C C C C C C C C C
Consensus(6098)								Section 69
(6189) 6189	6200	6210	6220	6230	6240	6250	6260	6279
SEQ ID NO 11(6189) CTGGCTAACGTGGTGAAACCCTGTCTCTACTAAAATACAAAAATTAGCCGGGCGTGGTGGCGGCGCCTGTAGTCCCAGCTACTCGGGA SEQ ID NO 4(4255)	CTAACGTGGTGAAA	CCCTGTCTCTA(CTAAAAATAC	AAAAAATTAGO	CCGGGCGTGG	166C666C6C	CIGIAGICCCAGCIAO	CTCGGGA
SEQ ID NO 16 (1)								
SEQ ID NO 17 (367)								
Consensus(6189)								

align SEQID#4 against SEQID#11.apr

Section 70 6360 6370	GCGACAGAACG	6450 6461	ATGTTGGCAGT	10 6552 TCTAATTAACC
6350	ACTCCAGGCCTGG	6440	TAAGCTAAACAA	6530 6540 CICACIGIGGGGIIC
6340	TTGCCCCAATGC	6430	AAAICAIGAACA	8520 CACTGTAGACCC
6330	GTCAGCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	6420	GAAATAGAGCCA	0TCCATGTCCTC
6320	GGAGCTTGCA 	6410	AATACCAGCA(CA(CA(CA(CA(CA(CA(CA(CA(CA(CA(CA(CA(C	6500 GAACACIGCA(
6310	CTCAGGAGGC	6400	AGGAAATGCC	CTCTTAACTA
6300	ATGGTGTGAAA	6390	GAACAAAACAAA	6480 A G A G A G C A G A
6290	3AGGCAGGAGA	6380	TCCGTCTCAGA	6470 CCTAGIGGITAA
(6280) 6280	SEQ ID NO 11(6280) SEQ ID NO 4(4255)	(6371) 6371	SEQ ID NO 11(6371) AGACTCCGTCTCAGAACAAAAGGAAATGCCAGTACCAGCAGAAATAGAGCCAAATCATGAACATAAGCTAAACAAATGTTGGCAGT SEQ ID NO 41(4255)	SEQ ID NO 11(6462) 6462 6470 6540 6550 65

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Section 73 6610 6620 6630 6643	ICATCTGTAGAAGGGGT		SEQ ID NO 41(6644) GITTACTTTATAGGCTTACTGTGAGGTTTACTACTGTATTTGTAAAGGCTTCCAAAAGAGTTTGTTAAAC SEQ ID NO 4(4255)	6790 6800 6810 6825	SEQ ID NO 11(6735) ACTTAAGAACTGATTTACTTGCATCTAAACTGACAGCTCTCCAATAACTGGAAATGATCAAGCCTGGAATATAAGCAGGTCTACA SEQ ID NO 4(4255)
0099	CGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG	0699	ACTGTATTTGT	6780	AATAACTGGAA
6590	TTCCTTAAGT	6680	ATGAGTTACT?	0//9	GACAGCTCTC7
6580	TCTTAAGGCA	0299	TGAGCATTAA	6760	CATCTAAAACT
6570	CCAGTGGCAG	0999	AGGCTTACTG	6750	GATITACTIG
33 6560	TGTTACTTA	4 6650	TTACITIAT	35 6740	TTAAGAACT
(6553) 6553	SEQ ID NO 11(6553) CCTGTTACCTTACCAGTGGCAGTCTT SEQ ID NO 4(4255)	(6644) 6644	SEQ ID NO 11(6644) GTITACTT SEQ ID NO 4(4255) SEQ ID NO 13 (306) SEQ ID NO 16 (1) SEQ ID NO 15 (558) SEQ ID NO 17 (367) SEQ ID NO 17 (367)	(6735) 673	SEQ ID NO 11(6735) ACTTAAGAACTGA SEQ ID NO 4(4255) SEQ ID NO 13 (306) SEQ ID NO 16 (1) SEQ ID NO 16 (58) SEQ ID NO 17 (367)

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align SEQID#4 against SEQID#11.apr

(6826) 6826	6840	6850	6860	6870	6880	0689	0069	Section 76 6916
SEQ ID NO 11(6826) TGAAGGCAAAATGTTCGTTTTTTTTTTTTTTTTTTTTTT	GGCAAAATGTTCGT	TH CHH H CHH CH H CHH H CH C	AGCCCTGTGC 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	CTAGATCAAT	ATCTAGTGAT	CATGCTCAA	IGITCAGCCCTGTGCCTAGATCTAGTGATCATGCTCAAGAAATATTGTTGAATGAA	IGAATCAA
(6917) 6917	06930	6940	6950	0969	6970	6980	0669	7007
SEQ ID NO 11(6917) TGAACCTACCGAGGTAGTTACATAAAAGAGTTCTGCATGAGTACAAATCTGGGCAAAGTGACCTCCCAAGGAAATTTCCACTT SEQ ID NO 4(4255)	CCTACCGAGGTAGTT	ACATAAAAGAG	TTCTGCATGA	GTACAAATCT	GGGCAAAGTG	ACCTCCAAG	GAAATTICCACTTT	TTAGATTCT
(7008) 7008	7020	7030	7040	7050	7060	7070	7080	Section 787098
SEQ ID NO 11(7008) GTGATTTCCTTAAGGAACTGATAAA SEQ ID NO 4(4255)	TTTCCTTAAGGAACT		GTGATACAAT	TGGTGTGATACAATGTAAAAATGTGCCTATATGATTTGAGAAAAACTTAT	GTGCCTATAT	GATTIGAGA	T T T T T T T T T T T T T T T T T T T	CTCTCCTTCTCCTCTTCTTCTTCTTCTTCTTCTTCTTCT
Consensus(7008)								

align SEQID#4 against SEQID#11.apr

Section 79 7189	Section 80	7280	CCTTT	Section 81 7371	
		7270	TTCTTTGT	7360	TCTTTCTTTTCTTTTTTTTTTTTTTTTTTTTTTTTTTT
7170		7260	CHILCHICCI	7350	TGTTTTTCTT
7160		7250	CTTTCCTTT	7340	H
7150	CCTTCCTTCCTTCCTCCCTCCCTTCCTTCCTTCCTCCCTCCCTTCCTTCCTTCTTTT	7240	CTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT	7330	CCTTTCTTTCTTTCTTTCTTTCTGCCTTTCTTTCTCTTTGTTTT
7140		7230	TTCTTTCTTT	7320	
7130		7220	CTTTCTTTCT 	7310	
7120	H	7210	TTCTTTCTTT	7300	TCTCTGTGTCCT
7110		7200	CITTCTTTCT	7290	
6602 (6602)	SEQ ID NO 11(7099) ITITICCITICCITICCITICCICCICCICCICCICCICC	(7190) 7190	SEQ ID NO 41(7190) CITTCITICITICITICITICITICITICITICITICIT	(7281) 7281	SEQ ID NO 11(7281) CTTTCTTTCTTTCTTTCTTCTCTCTCTGTS SEQ ID NO 4(4256)
	SEQ ID NO 11(7099) SEQ ID NO 4(4256) SEQ ID NO 13 (306) SEQ ID NO 16 (1) SEQ ID NO 15 (558) SEQ ID NO 17 (367) Consensus(7099)		SEQ ID NO 11(7190) SEQ ID NO 4(4256) SEQ ID NO 13 (306) SEQ ID NO 16 (1) SEQ ID NO 15 (558) SEQ ID NO 17 (367) Consensus(7190)		SEQ ID NO 11(7281) CT SEQ ID NO 4(4256) SEQ ID NO 13 (306) SEQ ID NO 16 (1) SEQ ID NO 15 (558) SEQ ID NO 17 (367) Consensus(7281)

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Section 82	6G T C T C C C C C C C C C C C C C C C C	7553	F 50 0 1	IBCCCI	 TGCCCT	Section 84	AGCTGC AGCTGC	0 0 0 0 4	 AGCTGC
22	A A B B B B B B B B B B B B B B B B B B	7540	TACAGITICATATCICCAGGCCTTTCATIGGGTCAGGTTGGCATTTGGCTGCCCT	IGGCATITIGG			CIGGGCGIIIC CIGGGCGIIIC	CAGAATUTGCGCAGDAGITCCIGGGGGTITCAGG	
0.44	AGTGAAGCAC	7530	TGGGICAGGI	TEGGETCAGGT	 TGGGTCAGGT	0000	GCAGCAGIIC GCAGCAGIIC	 ccaccaett	
0072	TAAACAGGAA	7520	GGCCTTTCAT	SGCCTITCATISGS	GGCCTTTCAT	0,000	CAGAAICIGC CAGAAICIGC	cagaatcrec	
0072	3TTAAAAGGT	7510	CATATCICCA CATATCICCA	CATATCICCAGG		0001	/OUO IGAAGAAAT IGAAGAAAAT	 caagtgaagaaat	 IGAAGAAAAT
7440	CCTTTTCTA	7500	TTTACAGITT ET	.T.E.I.—————————————————————————————————		1000	ASASCICASG' SABACICAAG'	 AAACICAAG	
	TAGATGAATG(7490	TCT			7000	JOON NGGRAAGARAJ RGGRAAGARAJ		
7900	CATGTCTGT CATGTCT CATGTC	7480	STTCTTAATC.			2570	/O/O AGTGAAAATAA AGTGAAAATAA	AGICAAAAAA	
7300	TTAAGCAGA(7470	ATCTCCACAT(0000	JOSO STGTGTGACA STGTGTGACA	TCTCTCACAL	
0767 (0767)	SEQ ID NO 11(7372) TICCTTTAAGCAGACCATGTCTGTT SEQ ID NO 44256)	(7463) 7463	SEQ ID NO 11(7463) AGTCATCTCCACATGTTCTTAATCATTATCT SEQ ID NO 4(4256)	SEQ ID NO 16 (1)	SEQ ID NO 15 (558) SEQ ID NO 17 (367) Consensus(7463)	7707 / 7707 /	(1934) (2934) (2934) (2934) (2934) (2934) (2934) (2934) (2934) (2934) (2934) (2934) (2934) (2934) (2934) (2934 SEQ ID NO 11(7554) TTATGTGTGTGTGAAATAAGGAAAGAAAAAAAAGTGAAGTAAAAAA	SEQ ID NO 13 (306)SEQ ID NO 16 (51) TRAISISISISSAAGISAAAIAA SEQ ID NO 16 (51) TRAISISISISSAAGISAAAIAA SEO ID NO 15 (558)	SEQ ID NO 17 (367)
	SEO I SEO I SEO I SEO I SEO I		SEQ I	SEQ	SEQ		SEQ I	SEQ	SEQ

Section 85 7735	TIAIC		ATTTATC Section 86	7826	(3 () (4 () (3 () () () () ()	(9 3 (9 (9	TGGGAG	7917	000000	1	0 0 0 0 0 0 0 0 0
Se	ATTCAT		ATICAT	5	0 0 0 0 4 0 0 0 0 0		TCACCT		CABABI	 Carra	 CAAAAT
7720	SEQ ID NO 11(7645) TECCCACATCACCTGCCTCATCAAGCCCCAGCATCCATCTTGCTCATCTTACACCCTGTGTGCATGACAGGCCCACCATTCATT	SEQ ID NO 13 (30b)	DID NO 17 (367)	7810	SEQ ID NO 11(7736) AGASCAAAGGGTGTGGGTTGTGGTTGAGGGGGGGGGGGGG		GITCACCCCCTACTIAGCCAGATATACAAGAATATCTGCACGGATGACCTGCCTCACCTGGGAGGAGGAGGAGAGAATATCTGCACGGATGACCTGCCTCACTGGGAGAGAATATCTGCACGGATGACCTGCCTCACTTACAGAATATCTGCACGGATGACCTGCCTCACTTACAGAATATCTGCACGGATGACCTGCCTCACTTACAGAATATCTGCACGGATGACCTGCCTCACTGCTCACTGCACGGATGACCTGCTCACTGCTCACTGCACGGATGACCTGCTCACTGCTCACTGCACGGATGACCTTACACTACACTACACACGGATGACCTGCTCACTACACTACACACGGATGACCTACACTACACACAC	7900	SEQ ID NO 11(7827) CTCAGAGGAGGTCAGGATTCCATTACTATCGCACCAAGGACAGATCTCCCAGGAAGACAGAGAAAAGACTAACTGCCCGCAAAATCTCCC SEQ ID NO 4(4578) CTCAGAGGAGCTCAGATTCCATTACTATCGCACCAAGGACAGATCTCCCAGGAAGAATGACAGAAAAAGACTAACTGCCCCAAAATGTCCC		
	GACAGG	1 0 1 1 2 1 1 1 2 1 1 1 2 1 1 1 2 1 1	 Gacagg		GGATGA	55 15 1 1 1 1 1 1 1 1 1	 GGATGA	7	ACTAAC ACTAAC	 actari	 actaac
7710	GTGCAT	GTGCAT	GTGCAT	7800	CTGCAC	TOTO	CIGCAC	7890	GAAAAG	GAAAAG	 GAAAAG
7700	SCCTGT	CCTGT.	CCCTGT	0	SAATAT	3AATAT	SAATAT		ATGACA	47GACA	 ATGACA
77	TTACA	TTACA:	TTACA	7790	ATACAA ATACAA	 atacar 		7880	SCAAGA	TCAAGA	 3CAAGA
7690	SCICATO	3CTCAT(GCICAI	7780	CAGA E		CAGAT	7870	STOCCAC	TCCCAC	TCCCA(
	TCCTT	H	TCCLL	,,-	CTTAG	1		78	ACAGAT.		 ACAGAT(
7680	ATCCATO TCCATO	TCCAT		7770		CACCCCCC - TACCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	CCCCIA	7860	7022007 7022007	 :caage	 :CAAGGA
7670	CCAGC	CCAGC?			TTCAC	{ 	TICAC		TOBOAC TOBOAC	TCGCAC	TCGCAC
.92	CAAGCC		TCAAGCC	7760	12010 1010 1010 1010 1010 1010 1010 101	E E E E E E E E E E	TICIGG	7850	TIACIA	TIMCIR	TTACTA
7660	CCTCAT	CCTCAT		7750	CCACIA	SEQ ID NO 13 (308)	OID NO 17 (367)	9	ATTOCA	SEQ ID NO 13 (306)	JID NO 17 (367)
	CACCTG	CACCIG 	SEQ ID NO 17 (367)	7	SOTOTO		GCTCTC	7840	GCTCAG	GCTCAG	 GCTCAG
7650	CCACAT		CCACAT		SCARAG	SEQ ID NO 13 (306) SEQ ID NO 16 (233) AGAGGAAAGG SEQ ID NO 15 (558)	 3CAAAG		408008 408008	SEQ ID NO 13 (306) SEQ ID NO 16 (324) CTCAGAGGAG SEO ID NO 16 (669)	SEQ ID NO 17 (367) SEQ ID NO 17 (367) Consensus(7827) CTCAGAGGAG
(7645) 7645 7650	(45) T.T.C. (96) T.T.C.	SEQ ID NO 13 (306) SEQ ID NO 16 (142) TTCCCA SEQ ID NO 15 (558)	167) 145) TTC((7736) 7736	36) AGA 87) AGA(SEQ ID NO 13 (308) SEQ ID NO 16 (233) AGAGG SEQ ID NO 15 (558)	SEQ ID NO 17 (367) Consensus(7736) AGAG	(7827) 7827	27) CTC. 78) CTC.	.06) (24) ⊜⊺⊖. 50)	20) 167) 127) CIC
92)	NO 11(76) NO 4(43)	NO 13 NO 16 (1 NO 15 (5	NO 17 (3 sensus(76	(77)	NO 11(77 NO 4(44	NO 15 NO 15 S 65 S 65	NO 17 (3 sensus(77	(78	NO 11 (78) NO 4(45	NO 13 NO 15 (3)	NO 17 (3 Sensus(78
	SEQ ID SEQ IE	SEQ D SEQ D	SEQ ID Cons		SEQ ID SEQ IE	SEQ D SEQ D	SEQ ID Cont		SEQ ID SEQ II		SEQ ID

Section 91 8281	AATCAAT AATCAAT	4.8.4.2.2.8.2. 	 AATCAAT Section 92	8372	1991TCB	ARRITCA 	 AAATTCA Section 93	8463	CTTTCTC		 FITICIC
8270	TTGACATEL TTGACAFIE	TIGACATITA	TIGACATITA	8360	TATAGAAGG!	TATAGAAGG2 	TATAGAAGG	8450	TTATGCCIG	Trarscers	TIAIGCCIG
8260	CCTTCAAATC CCTTCAAATC	CCTTCABATC 		8350	CAAICCAGAC Caaiccagac	ITCIIIIACAAICCAGACIAIAGAAGGAAAIICA	CAATCCAGAC	8440	iaacggaagt Iaacggaagt	CCITACACCTAACGGAAGTITATGCCIGIT	 TAACGGAAGT
8250	AGAAGTTOTT AGAAGTTOTT 	AGAAGTICIT		8340	TITICITITA ESTCITITA	-8-4		8430	CIGACCAATICCCACCICIGCCITACACCIAACGGAAGIITAIGCCIGIT CIGACCAATICCCACCICIGCCITACACCIAACGGAAGTITAIGCCIGIT	SCCITACACC	
8240	ATAAGCAACC 4TAAGCAACC 	YTAAGCAACC. 	ATAAGCAACC	8330	CCTGAAGGAT	CCTSAAGSAT		8420	receacerer receacerer	CCCACCICI	
8230	XITIAGCICG XIITAGCICG 1	ELTERGCICO		8320	SCTATCTCTG(TCCTAIGAAGCIAICTCTGCCIGAAGGAII		8410	ACTGACCAAT ACTGACCAAT	ACTGACCAAT	
8220	AGGATTATTCK AGGATTATTCK	AGGATTATTO	 AGGATTATICO	8310	TTCCTATGAAGCTATCTCTGCCTGAAGGATTTTTCTTTTACAATCCAGACTATAGAAGGAAATTCA TTCCTATGAAGCTATCTCTGCCTGAAGGATTTTTCTTTTACAATCCAGACTATAGAAGGAAATTCA	1-4		8400	TCAGAGTTTT/	CAGAGITIL	
8210	rggggaaaat rggggaaaat 	IGGGBAAAAI.	 TGGGGAAAATA	8300	GGAAAACTGT GGAAAACTGT	SGAAAACIGI	GGAAAACIGI	8390	CCTCCATTGG	CTCCATIGG	CCTCCATTGG
8200	rcasicaras rcasicaras 	TCAGICATAG		8290	ATTOATTTT ATTGATTTT	ATTGATTTTT		8380	EGGACTITCA EGGACTITCA	IGGACTITCA	
(8191) 8191	SEQ ID NO 11(8191) TATATICAGICATAGICGGGAAATAGGATTATICCITTAGCICGATAAGCAACCAGAAGITCTICCITCAAATCITGAGATTIAATGAAT SEQ ID NO 4(4942) TATATICAGICA FAGIGGGGAAAATAGGATTATICCITTAGCITCGATAAGCAACCAGAAGITCITCGATTGAGAATTITGAATGAAT SEO ID NO 13 (306)	SEQ ID NO 16 (688) TATATICASICATAGIGGGAAAAIAGGAITAITCCIITASCICGAIAAGCAACCAGAAGIICIICCIICAAAICIIGACATIIAAICAAI SEQ ID NO 15 (558)	SEQ ID NO 17 (367)	(8282) 8282	SEQ ID NO 11(8282) CAGAAATTGATTTTTGGAAACTGTTTCCTATGAAGCTATCTCTGCCTGAAGGATTTTTCTTTACAATCCAGACTATAGAAGGAAATTCA SEQ ID NO 4(5033) CAGAAATTGATTTTTGGAAACTGTTTCCTATGAAGCTATCTCTGCCTGAAGGATTTTTTTT	SEQ ID NO 16 (779) CAGARAITGAITITTGGAAAACIGI SEQ ID NO 15 (558)	SEQ ID NO 17 (367)	(8373) 8373	SEQ ID NO 11(8373) CAACCTEGACTITICACCTCCATTGGTCAGAGTTTTACTGACCAATTCCCACCTCTGCCTTACACGTAACGGAAGTTTATGCCTGTTTT SEQ ID NO 4(5124) CAACCTGGAGTTTCACCTCCATTGGTCAGAGTTTTACTGACCAATTCCCACCTCTGCCTTAGACCTAACGGAAGTTTATGCCTGTTTT SEO ID NO 13 (206)	SECTION 15 (909) SECTION 15 (909) SECTION 15 (569)	SEQ ID NO 17 (367)

Section 94 8554	TGACCT	I	TIGACCT	8645	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		 AGAGGTC Section 96	8736	ATTTA ATTTA	7. T. T. 7. 7. 7. 7. 7. 7. 7. 7. 7. 7. 7. 7. 7.	 ATTTTA
8540	GGTTGTTATTATTAAGCATCTTTTATTTTGTGGCCTCTGATTACATGGTCCCCTAAATTTTGACCT GGTTGTTATTATTAAGCATCTTTTATTTTGTGGCCTCTGATTACATGGTCCCCTAAATTTTGACCT	GGTIGTTATTATTAAGGATGITTTATTTTGIGGCCTCTGAATTACATGGTCCCCTAAATTTTGACCT		8630	ttaacatattaataatattteetttatetecaatatcttaecateteaatateaeateteaattaagacaggete ttaacatattaataatattteettiateteaeatatettageateteaattaagacaee	TAGCATGTATCAATTAAGACAGGTC	TATGTGTCAATATCTTAGCATGTATCAATTAAGACAGAGGTC	8720	TATTAGGATTCAGAGATATTAAGAGATTCTCCCAGGATCACAGITAGGTAACAGAGCTGGATTTTA TATTAGGATTCAGAGATATTAAGAGATTCTCCCAGGATGACAGTTAGGTAACAGAGCTGGATTTTA	CCCAGGATCACAGTTAGGTAACAGAGGTGGATT	
8530	GATTACATO GATTACATG	GATTACATG	 .GATTACATG	8620	TIAGCATGT TIAGCATGT	TTAGCATGE	TIAGCAIGI	8710	CACAGITAG	CACACTIAG	CACAGITAG
8520	TOLOGOCOLOL	.16168CCTCT	TGTGGCCTCT	8610	TGTCAATATC TGTCAATATC	TAIGIGICAATATOT 	: TGTCAATATC	8700	CICCCAGGAI	11	CTCCAGGAT
8510	GGTTGTTATTATTAAGCATCTTTTATTT GGTTGTTATTAAGCATCTTTTATTT	.TCTTTTATT	 TCTTTTATT	8600	TITGITIALE		TITGIIIAIG	8690	TTAAGAGATI TTAAGAGATI	TAGGATTCAGAGATATTAAGAGATTC	 TTAAGAGATT
8500	TIATTAAGCA TTATTAAGCA	TIATIAAGCA 	 TTATTAAGCA	8590	TTAACATATTAATATT TTAACATATTAATAATT	TAACATATTAATAATAT 	TAACATATAATATTTTGTT	8680	TATTAGGATTCAGAGATATTAAGAGAT TATTAGGATTCAGAGATATTAAGAGAT	TTCAGAGATA	 TTCAGAGATA
8490	ATGGTTGTTA ATGGTTGTTA	ATGGTIGTTA 	ΙÜ	8580	ICITAACATA ICITAACATA	-4	[⊢	8670	AATATTAGGA AATATTAGGA	64 84 64	 AATATTAGGA
8480	ACAGITACAA ACAGITACAA	ACAGTTACAA 	 CCAACAGTTACAA	8570	TGGTAAAATT TGGTAAAATT	TGGTAAATT 	 IGGTAAAATT	8660	TTTGAAAGAG TTTGAAAGAG	TTTGBAAGAG	 TTTGAAAGAG
8470	SATACCCCA			8560	ACABABGAT ACABAGAT				GRICICIT		GITCICIT
(8464) 8464	SEQ ID NO 11(8464) TECACATACCCCAACAGITTACAAAT SEQ ID NO 4(5215) TECACATACCCCAACAGITACAAAT SEC ID NO 49 (2005)	SEQ ID NO 15 (308)	SEQ ID NO 17 (367)	(8555) 8555	SEQ ID NO 11(8555) AATCACAAAAGATTGGTAAAATTTC SEQ ID NO 4(5306) AATCACAAAAGATTGGTAAAATTTC SEC ID NO 19 (2005)	SEQ ID NO 15 (309)	SEQ ID NO 17 (367)	(8646) 3646	SEQ ID NO 11(8646) TTAACGTTCTCTTTTTGAAAGAAA SEQ ID NO 4(5397) TTAACGTTCTCTTTTTGAAAGAGAA SEQ ID NO 40, 2009.	SEQ ID NO 13 (500)SEQ ID NO 16(1143) TIBACGTICICITITIGAAAGAGAA SEO ID NO 46 (468)	SEQ ID NO 17 (367)SEQ ID NO 17 (367)

align SEQID#4 against SEQID#11.apr

1000	8750	8760	8770	8780	8790	8800	8810	8827
SEQ ID NO 11(8/3/) GTCCAGGTCTGTCTACAGGTCTAACGT SEQ ID NO 4(5488) GTCCAGGTCTGTCTACAGGTCTAACGT SEQ ID NO 13 (306)	KGGTCTGTCTACAG KGGTCTGTCTACAG	CTCTAACGTAT CTCTAACGTAT 	ATACACCTT ATACACCCTT	TGTATAACAT TGTATAACAT 	GTCACGAATI GTCACGAATI 	CAGCATAAAC CAGCATAAAC 	SEQ ID NO 11(8737) GECCAGGECTATACAGCECATATACACCCETTGEATACATGECATGE	TAAGTCA TAAGTCA
SEQ ID NO 16(1234) GICCAGGICTGICIACAGCICTAACG SEQ ID NO 15 (558)	AGGTCTGTCTACAG	i1	AIATACACCCTT 	IGTATAACAT	GICACGAATI	CAGCATAAA	TGIATAACAIGTOACGAATICAGOATAAAGGGATCTICAGIGAICIAAG	TAAGTCA
SEQ ID NO 17 (367)		;crciaacgiai	ATACACCCIT	TGTATAACAT	GICACGAATI	: :cagcataaa		TAAGTCA Section 98
(8828) 8828	8840	8850	8860	8870	9880	8890	8900	8918
SEQ ID NO 11(8828) GGGGTCAGCAACCTTTTCTAAAAAGGACCAAATAGTAATA SEQ ID NO 4(5579) GGGGTCAGCAACCTTTTCTAAAAAGGACCAAATAGTAATA SEQ ID NO 13 (306)	CAGCAACCTITTC CAGCAACCTITTC	TAAAAAGGACC TAAAAAGGACC 	AAATAGTAAT	ATTICAGGCTT ATTICAGGCTT	TIGIGGACCC TIGIGGACCC	TGTGGACCCTATGGTCTCT TGTGGACCCTATGGTCTCT	EQ ID NO 11(8828) GGGGTCAGCAACCTTTTCTAAAAGGACCAAATAGTATTTCAGGCTTTGTGGACCCTATGGTCTCTATCATAACTGTTCAAATCACCA SEQ ID NO 4(5579) GGGCTCAGCAACCTTTTCTAAAAGGACCAAATAGTAATATTTCAGGCTTTGTGGACCCTATGGTCTCATCATAACTGTTCAAATCACCA EQ ID NO 13 (306)	ATCACCA ATCACCA
SEQ ID NO 16(1325) GGGSTCASCAACCTTTTCTAAAAAS SEQ ID NO 15 (558)	CASCAACCITITC	Trarasgrc 	GACCAAATAGTAAT.	AITICAGGCT	TIGIGEROCO	TATGGTGTG	TAICATAACTGTTCAAAI	AICACA
SEQ ID NO 17 (367)	CAGCAACCITITC	TAAAAAGGACC	; AAATAGTAATATT	ATTTCAGGCT	TIGIGGACCC	CIATGGTCTC	TCAGGCTTTGTGGACCCTATGGTCTCTATCATAACTGTTCAAA	TCAAATCACCA Section 99
(8919) 8919	8930	8940	8950	8960	8970	8980	8990	6006
SEQ ID NO 11(8919) TGTAGTGTAAAAGGAGCCATAAGCAAAATATAAACTAACGAATGTGGCTGT SEQ ID NO 4(5670) TGTAGTGTAAAGGAGCCATAAGCAAATATAAACTAACGAATGTGGCTGT SEO ID NO 13 (306)	STGTAAAAGGAGGC STGTAAAAGGAGGC	ATARGCAAAAT	ATAAACTAAC ATAAACTAAC	GAATGTGGCT GAATGTGGCT	GITTIATGGGATTIT	ATTTTTT SATTTTTTT	aatataaactaacgaatgtggctgtttatgggatttttttt	ACAAAAGCAG ACAAAAGCAG
· čina	HETAAAGGAGGC	82,	AIATAACTAACGAATGTGGCTGT	GAATGTGGCI	¥ EE	TGGGATTTTTTT	ITITAACTOTITATTIAGA	TACARAGGAG
SEQ ID NO 13 (332)SEQ ID NO 17 (367)								

align SEQID#4 against SEQID#11.apr

Section 100	9100	7.67.6ACT 1.67.6ACT 1.07.6ACT	TST875	 STGTGACT Section 101	9191	GTGAAAT	CEESAAT	Section 102	9282	TIAGGCA TIAGGCA	TERECE	 :: :TTAGGCA
	0606	CATTIAGAC CATITAGAC	CATTAGAS	CATITAGAC	9180	CIGGIGITANIGALAAGIGAAAT CIGGIGITAALGALAAGIGAAAT	CTGGTGTTAATGATAAG	TAATGATAA	9270	ACTICIESC ACTICIESC	ACTTCTGGG	
	0806	TATGGACAA TATGGACAA 	TATGGACAA	TATGGACAA	9170	GTCT6GTGT GTCTGGTGT 1	## I ## ## ## ## ## ## ## ## ## ## ## ##	GICIGGIGI	9260	AATGICIGG	AATGTCTGG 	
	9070	SCCATAGITCICIGACCCCIGACCIGAGAAAICITATTITATGGAGAACATITAGACTGIGACT SCCATAGIICICIGACCCCIGACCIGAGAAAICITATITATGGACAACATITAGACIGIGACT	GCCATAGTTOTOTGACCCTGACCTGAGAAATCTTATATTTTATGGACAACATTTAGACTGTGA		9160	TCAACTGAAGGTCAAGGCTGGAGTTCTGAAAGCAAAGAGCTGTCTGGTGTTAATGATAAGTGAAAT TCAACTGAAGGTCAAGGCTGGAGTTCTGAAAGCAAAGAGCTGTCTGGTGTTAATGATAAGTGAAAT	ICAACTGAAGSICAAGGCIGGAGTICISAAASCAAAGACTGT	 TCAACTGAAGGTCAAGGCTGGAGTTCTGAAAGCAAAGAGCTGTCTGGTGTTAATGATAAGTGAAAT 	9250	TAAGAAGCACACAAATAATGACCATAGACTCCTGAACAAGAATGTCTGGACTTCTGGCTTAGGCA	AAGAAGDADAAAGAATAATGACCATAGACTCCIGAACAAGAATGTCTGGACTTCTGGGC	
	0906	ACCTGAGAAA ACCTGAGAAA 	ACCTGAGAAA	 accigagaaa	9150	AGTICTGAAA AGTICIGAAA 	AGTICIGAAA	AGIICIGAAA	9240	ACCATAGACT ACCATAGACT	ACCATAGACT	
	9050	01020000000000000000000000000000000000	TEACCCCTG	CTGACCCCTG	9140	FCAAGGCTGG TCAAGGCTGG	ECAAGGCTGG	 ICAAGGCIGG	9230	AAGAATAATG AAGAATAATG		 AAGAATAATG.
	9040	CATAGITOR CATAGITOR	CATAGITOI	CATAGIICI	9130	AACTGAAGG AACTGAAGG	AACTGAAGG	AACTGAAGG	9220	AGAAGCACA.	AGAAGCACA)	
	9030	ACTTATGGGC ACTTATGGGC	ACTIATEGEC	ACTTATGGGC	9120	AAGCICIGIC AAGCICIGIC	AAGCICIGIC	AAGCTCTGTC	9210	CCCAGIIAIA	8-4	1
	9020	ATCAGAACTC ATCAGAACTC 	ATCAGAACTC	ATCAGAACTC	9110	TAAGAACAAG TAAGAACAAG 	Taagaacaag 	TAAGAACAAG	9200	GTTAGAAGAT GTTAGAAGAT	GIIAGAAGAI	 GTTAGAAGAT
	(9010) 9010	SEQ ID NO 11(9010) GTGGCAGATCAGACTCACTTATGG SEQ ID NO 4(5761) GTGGCAGATCAGAACTCACTTATGG SEQ ID NO 13 (306)	SEQ ID NO 16(1507) STGGCAGATCAGAACTCACTIATGG	DID NO 17 (367)	(9101) 9101	SEQ ID NO 11(9101) TGCCAAGTAAGAACAAGAAGGTCTG SEQ ID NO 4(5852) TGCCAAGTAAGAACAAGAAGGTCTG SEQ ID NO 13 (306)	SEQ ID NO 16(1598) TGCCAAGTAAGAACAAGAAGCTCTG SEQ ID NO 15 (558)		(9192) 9192	SEQ ID NO 11(9192) AGTTAAAGTTAGAAGATCCCAGTTA SEQ ID NO 4(5943) AGTTAAAGTTAGAAGATCCCAGTTA SEC ID NO 19 (206)	SEQ ID NO 13 (300)	SEQ ID NO 17 (367)SEQ ID NO 17 (367)
		SEQ ID NO 11(9010) 6166 SEQ ID NO 4(5761) 616 SEQ ID NO 13 (306)	SEQ ID NO 1	SEQ ID NO 17 (367) Consensus(9010) GTG		SEQ ID NO 1 SEQ ID NO 1	SEQ ID NO 16(1598) SEQ ID NO 15 (558)	SEQ ID NO 17 (367) Consensus(9101)		SEQ ID NO 1	SEQ ID NO 1	SEQ ID NO 1 Consensus

align SEQID#4 against SEQID#11.apr

9373	CCTCA	8; 0 H 0	TICCICA Section 104				
0986	aaagtatiti aaaagtatit	AAAAGTATTT 	 AAAAGTATTTT Sec	9458	TAAAIGCCAG TAAAIGCCAG	TAAATGCCAG	
9350	TACCTAATCTCTCCAGGCCTCCATTTTCTTATCATTAAATGAAGATAATAAAGGTATTTTCCTCA TACCTAATCTCTCCAGGCCTCCATTTTCTTATCATTAAATGAAGATAATAAAGGTATTTTCCTCA	ATGAAGATAAT 	 ATGAAGATAAT	9440	acccatgicaagcacatagaatagggccagcctatattaatttatcaataatgccag acccatgicaagcacatagaatagggcccagcctatattaatttatcaataaatgccag	TAATTTATCAA 	
9340	CTIATCATTAR CTIATCATTAR	CITAICATIAA 	CTTATCATTAA	9430	CCAGCCIATAT CCAGCCIATAT	CCASCCIATAT	
9330	CCICCATITI	CCTCCATITIC	CCICCATITIC	9420	AGAATAGGGC AGAATAGGGC	AGAATAGGGGC	
9320	rererecass. rererecass	TOTOTOG(TCTCTCCAGG	9410	TCAAGCACA I. TCAAGCACA I.	TCARGCACAT	TCAAGCACAT
9310	AGTTACCTAA AGTTACCTAA	AGTIACCTAA	AGITACCIAA	9400	CTAACCCATG	CIBACCCATG	CIAACCCAIG
0086	GICCAGGCCA	GTCCAGGCCA	 GICCAGGCCAA	0686	ATAAACTGAG ATAAACTGAG	ATAAACIGAG 	
9290	TGTTGTATG	TCTTCTVTC	 TGTTGTATGGT	9380	GCICTAAGAAT GCICTAAGAAT	GOISIAAGA	
(9283) 9283	SEQ ID NO 11(9283) CTCTTGTTGTTGGTCCAGGCCAAGTTACCTAATCTCTCCAGGCCTCCATTTGTTATCATTAATGAAGATAATAAAGTATTTTCCTCA SEQ ID NO 46034) CTCTTGTTGTTGTTGGTCCAGGCCAAGTTACCTAATCTCTCCAGGCCTCCATTTTCTTATCATTAAATGAAGATAATAAAGAATTTTCCTCA SEO ID NO 43 /2063	SEQ ID NO 15 (309) CTCTTGTTBTATGGTCCAGGCCAAGT SEO ID NO 15 (558)	SEQ ID NO 17 (367)	(9374) 9374 9380	SEQ ID NO 11(9374) GAGAGCIGIAAGAATAAACTGAGCTAACCCATGTCAAGCACALAGAATAGGGCCCAGCCTATATTAATTIATCAATAATGCCAG SEQ ID NO 4(6125) GAGAGCIGIAAGAATAAACTGAGCTAACCCATGTCAAGCACATAGAATAGGGCCCAGCCTATATTAATTA	SEQ ID NO 16(1871) GAGAGCIGIAAGAATAAACIGAGCIAACCCAIGICAAGCACAIAGAATAGGGCCCAGCCIAIAIITAIIIAICAATAAAIGCCAG SEQ ID NO 15 (558)	SEQ ID NO 17 (367)

EXHIBIT D

										Section 1
	1)	10	50	30	40	90	6	70	08.	91
SEQ ID NO 6 SEQ ID NO 13		GAATIGGIGA GAATIGGIGA	ACTIAGTAA! ACTIAGIAA!	AGCAGACGGC AGCAGACGGC	TCTCACCAATA TCTCACCAATA	AGGGCAGGC AGGGCAGGC	ATCATCCARTE ATCATCCAATC	TGTCGAAAC TGTCGAAAC	1) attigaattegtgaacttagtaaagcagacggctctcaccaataagggcaggca	ACAAAAAG ACAAAAAAG
Consensus		.ı) atttgaattggtgaacttagtaaag	 ACTTAGTAA?	AGCAGACGGC	TCTCACCAATA	AGGCAGGC?	 ATCATCCAATC	TGTCGAAAG		CAAAAAG Section 9
	(92) 92	100	110	120	130	140	150	160	170	182
SEQ ID NO 6 SEQ ID NO 13		(92) AGGAAGGGAAAATTIGCTICITITC	TGCTTCTTT.	ICTICITGAT ICTICITGAT	TICITGATCTAGIAIATCATCITCTCCIGCCCT	TOTICICIA	SCCCTIGGAIG	TGAGTGGG	TICITGATCTAGIATATCATCITCTCCTGCCCTIGGATGTGAGTGGGCCTTCAGACTTAAACCAGG ITCTTGATCTAGIATATCATCTTCTCCTGCCCTTGGATGTGAGTGGGGCCTTCAGACTTAAACCAGG	AAACCAGG
Consensus		AGGGAAAATT	TGCTTCTTT	 ICTTCTTGAT	CTAGTATATCA	TCTTCTCTG	SCCCTTGGATG	TGAGTGGGC	(1)	AAACCAGG Section 3
	(183) 183	190	200	210	220	230	240	250	260	273
SEQ ID NO 6	(183) AGIT	SEQ ID NO 6 (183) AGITACACCITIGGCITCCCIGGIT FO ID NO 13 (183) AGITACACCITITGGCITTCCCTGGTT	CTTCCCTGG	ITCICAGITC	SEQ ID NO 6 (183) AGITACACCTIIGGCIICCCIGGIICICAGIICIIIGGACIIGGAATIACACIGGCAGGIIIC SEO ID NO 13 (183) AGITACACCTITACACTITACATICAGATICIITAGACTIGGACTIGAATIACAACTACAAGATITA	ACTGAATTA(GGACITGGACTGAATTACACTGCCAGGTT	EBUCCECCEE	CICCAGOTO	
SEQ ID NO 16	(1)			*			10000000000000000000000000000000000000	7 1 5 1 5 1 1 1 1 1 1	2	9 1 9 1 9 1 5 1 5 1
Consensus	(183) AGIT	Consensus (183) AGTTACACCTTTGGCTTCCCTGGTT	CIICCCIGG	CICAGI	TITGGACIIGG	ACTGAATTA(CACTGCCAGGT	TICCIGGI	TCTTTGGACTTGGACTGAATTACACTGCCAGGTTTCCTGGTTCTCCAGCTTGCAGAGGCTGGC SATGGC Section 4	SAGATGGC — Section 4
	(274) 274	280	290	300	310	320	330	340	350	364
SEQ ID NO 6	(274) AGAT (274) AGAT	SEQ ID NO 6 (274) AGAICATGGGACITCITGGCCICCA SEQ ID NO 13 (274) AGAICATGGGACITCITGGCCICCA	CTTGGCCTC		TICATATCICC 	AGGCCTTTC?	% T T G G G T C A G G	TTGGCATT	TAAITGITTICATATCICCAGGCCITICATIGGGICAGGITGGCATTICGCTGCCCTTTATGIGG	:ATGTGTG
SEQ ID NO 16	(1)			(E 	TTTCATATCTCC	CATATOTOCAGGCCITTOATE	CORCECTOR	TIGGGATT	5-4 E	TOIG
COLUSATION	(<!--</b-->4) AGA1	CONSENSUS (Z/4) AGAICAIGGGACIICIIGGCCICCA) T T 2 2 2 1 1 1	IAAIIG	IIIICAIAICICC	CICCAGGCCIIICA	AIIGGGICAGGI	I GGCA I I	100001001	TAIGIGIG

SEQ ID NO 6 (365) TGAC SEQ ID NO 13 (306) SEQ ID NO 16 (60) TGAC	202) 202	380	380	400	410	420	2		455
EQ ID NO 16 (60)	TGACAAGTGA	ka aa ta agga a	LAGAAAAAAA	TCAAGTGAAG	SABATCAGAR	TCTGCGCAGC	AGTTCCIGG	SEQ ID NO 6 (365) I GACAAGT GAAAA TAAGGAAAGAAAAAAACT CAAGTGAAGAAAT CAGAATCTGCGCAGCAGTTCCTGGGGGTTT CAGCTGCTTCCCACAT En id no 12 (200)	TCCCACAT
Consensus (365)	TGACAAGTGA TGACAAGTGA	JID NO 18 (300)	 abgabababa abgabababa	TCAAGTGAAGI	 saaatcagaa aaaatcagaa	TCTGCGCAGC.	AGTICCIGG		TCCCACAT TCCCACAT Section 6
(456) 456	456	470	480	490	500	510	520	530	546
SEQ ID NO 6 (456) CACCTG	りょうひりょうりゅう	TAICAAGCCCC	MGCATCCATC	TCCLTGCTCA	ECTIACACCO	TGTGTGCATG	YCHOOOOBKOK	CATICALITALC	GAGCAAAC
SEQ ID NO 15 (309)SEQ ID NO 16 (151) CACCTGCCTCATCAAGCCCCAGCAT Consensus (456) CACCTGCCTCATCAAGCCCCAGCAT	CACCIGCOTC	 ORICAAGCCCC CAICAAGCCCC	JAGCATCCATCT	TCCTTGCTCAT	TCTTACACC	TGTGTGCATG	ACAGGCCGAC ACAGGCCCAC	CCATCICCIIGCICAICIIACACCCIGIGIGCATGACAGGCCCACCAIICATIIAICAGAGCAAAG CCAICICCIIGCICAICIIACACCCIGIGIGCAIGACAGGCCCACCAIICAII	GAGCAAAG GAGCAAAG Bection 7
(547) 547	547	260	570	580	280	009	610	620	637
SEQ ID NO 6 (547) GCTC SEQ ID NO 13 (306)	CHOCOTOLOU BOOKER	CIAIICIGGII	TICACCCCCCTA	CITAGCCAGA	IAIACAAGAA	TATCTGCACG	GATGACCIGC	()	() () () () () ()
EQ ID NO 16 (242) GCTCTCCCACTATTCTGGTTCACCC	GCTCTCCCAC	TATICIGGII TATICIGGII	CACCCCCTA	CTTAGCCAGA CTTAGCCAGA	FATACAAGAA IATACAAGAA	TATCIGCACG	GATGACCTGE GATGACCTGC	CICACCIGGGAG	TCAGAGGA
829 (838)	638	650	660	670	089	069	700	710	728
SEQ ID NO 6 (638) GCTCAGATTCCATTACTATCGCACC	GCTCAGATIC	CATTACTATO	GGACCAAGGA	CAGAICTCCC	AGCAAGAAIG	ACAGAAAAGA	CTAACTGCCC	aaggacagateteccagcaagaatsacagaaaagactaadtgececeaaaateteccatecaaaae	ICCARAR
SEQ ID NO 15 (303) SEQ ID NO 16 (333) GCTC Consensus (638) GCTC	GOTCAGATIC GCTCAGATIC	 CCATTACTATC CCATTACTATC	 Cecaccaasea Cecaccaagga	CAGATOTOCO!			 Ciaaacigoog Ciaacigooo	SECTIONO 13 (300)	TCCABABO TCCABABO

SEC DNO 6 (729) ACASTITCTCTTAATITCTCCCAAGAACCCAGATGIGACTGTCTCTCTAAGGACCTGAAAACTGGCCATTTCAGCTATTTAAATCCCORSONSON (729) ACASTITCTCTCCAAGAACCCAGAATCCACATTTCAGCTCTTTAAATCCCTTCTTAAATCTCTTTAATTTCTCCCAAGAACCCAAGAACTGGCCATTTCAGCTATTTAAATCCCTTCTTAAATTCTCTTTAATTCTCCCAAGAACCCAATTTCAGCTATTTAAATCCCTTCTTTAAATTCTCTTTAAATTCTCTTTAAATTCTCTTTAAATTCTCTTTAAATTCTCTTTAAAATTCTCTTTAAAATTCTCTTTAAAATTTTAAAATTCTCAACCGCCAATTTAAAATTCTCTTTAAAAATTCTCAACCGCCAAATTTAAAACTTTTGGTTGG
Section Sado 840 850 860 870 880 890 900
IAAAAAATCCAACCGCCAAAATAITAAACCATITIGGIIGGAAIGAIAACAIAAC
TAAAAAATCCAACCGCCAAAATATTAAACCATTTTGGTTGG
920 930 940 950 960 960 970 980 980 990 TGGAAAAAAAAAAATACTICTAAICAGGICAAAICACICTACCTITGGGAITCTAAATITACTCAAAITCTCAAAGAAATATATI TGGAAAAAAAAAAAAAAAAAATCAGGICAAAICACTCTACCTTIGGGAITCTAAATTTACTCAAAGAAATATATT TGGAAAAAAAAAA
TGGAAAAAAAAAATACTTCTAATCAGGTCAAATCACTCTACCTTTGGGATTCTAAATTTACTCATATTCTCAAAGAAATATTATT TGGAAAAAAAAAA
1010 1020 1030 1040 1050 1050 1070 1080 GIGGGGABAATAGGATTATTCCTTTAGCTCGATAASCAACCAGAAGTICTICCTTCAAATCTIGACATTTAATCAATCAGAAA
GIGGGGAAAAIAGGAIIAII

(109	(1093) 1093	1100	1110	1120	1130	1140	1150	1160	1170	1183
SEQ ID NO 6(1093) ATTTT SEQ ID NO 13 (306)	3) ATTT: 3)	TGGAAAAC 	SEQ ID NO 6(1093) ATTTTTGGAAAACTGTTTCCTATGA EQ ID NO 13 (306)	55	rcrecereaac	SGATTITCT	TITACAAICCA	KGACTATAGA 	GCTAICICICCCIOAAGGAITITICITITACAAICCAGACIAIAGAAGGAAATICACAACCIGGA	ACCTGGA
NO 16 (78) sensus(109)	8) ATTT 3) ATTTI	TTGGAAAAC TTGGAAAAC	SEQ ID NO 16 (788) ATTTTTGGAAAACTGTTTCCTATGA Consensus(1093) ATTTTTGGAAAACTGTTTCCTATGA		rcrecereaa rcrecergaa	SGATTITICI	TTTACAATCC! TTTACAATCC!	NGACTATAGA NGACTATAGA	AGCTATCTCTGCCTGAAGGATTTTTTTTTACAATCCAGACTATAGAAGGAAATTCACAAACCTGGA AGCTATCTCTGCCTGAAGGATTTTTCTTTTACAATCCAGACTATAGAAGGAAATTCACAAACCTGGA	ACCIGG. ACCIGG
(118	(1184) 1184 1190		1200	1210	1220	1230	1240	1250	1260	1274
D NO 6(118	4) CITIE	SACCICCATIGG	TCA	TITACIGAC	MATICCCAC	SICICOCCIIA	CACCIAACGG	ASITIAISC	TACIGACCAAITCCCACCICIGCCTIACACCIAACGGAAGITIAIGCCIGITTCICITCACALAC	ICIICACAIA
SEQ ID NO 16 (879) CTTTC Consensus(1184) CTTTC	9) CTTT(4) CTTT(ACCTCCAT	SEQ ID NO 15 (309)SEQ ID NO 16 (879) CITICACTICATIGGICAGAGITT Consensus(1184) CITICACCICCATIGGICAGAGITI	TTTACTGACC TTTACTGACC	AATTCCACK	CTCTGCCTTA	CACCTAACGG CACCTAACGG	AAGITIATGC AAGITIAIGC	TACTGACCAATTCCCACCTCTGCCTTACACCTAACGGAAGTTTATGCCTGTTTTCTCTTCACATAC TACTGACCAATTCCCACCTCTGCCTTACACCTAACGGAAGTTTATGCCTGTTTTCTCTTCACATAC TACTGACCAATTCCCACCTCTGCCTTACACCTAACGGAAGTTTATGCCTGTTTTCTCTTCACATAC Section 15	CACATAC CACATAC - Section 15
(127) D NO 6(1275)	(1275) 1275 1280 (1275) CCCAACAS	1280 NORGITACA	1290 IGGIIS	1300 ATIATTAAGC	77 K	1320 ITIGIGGCOI	1330 CIGALIACAIC	1340 3GTCCCCTRA	1350 TTG	1365 ICACAAA
SEQ ID NO 16 (970) SEQ ID NO 16 (970) CCCAA Consensus(1275) CCCAA	9) ====: 9) CCCA? 5) CCCA?		SEQ ID NO 15 (970)SEQ ID NO 16 (970) CCCAACAGTTACAATGGTTGTTAT Consensus(1275) CCCAACAGTTACAAATGGTTGTTAT	 ATTATTAAGG ATTATTAAGG		TTGTGGCCT	 CTGATTACATO CTGATTACATO	GGTCCCTAA		TCACAAA TCACAAA Section 16
(136	(1366) 1366		1380	1390	1400	1410	1420	1430	1440	1456
D NO 6(136	S) AGATI	TGGTAAAAT	FARCAS	ATTAATAATA	MITTELLIA	IGIGICAATA	TCTIAGCATG	MICRAITAR	TAATAATATTTTTGTTTATGTGTCAATAICTTAGCATGTATCAATTAAGACAGGGTCTTAACGTTC	AACGTT
SEQ ID NO 13 (306) SEQ ID NO 16(1061) AGATT	6) 1) agati		TICTIBACAT	ATIAATAAT		 IGTGTCAATA	TCTIAGCATG	 BICABITAB	SEQ ID NO 13 (306)	

AGAATATIASGATICAGAGATATTAASGAGATICTCCCAGGATCACAGTTAGGTAACAGAGCTGGAT AGAATATTAGGATTCAGAGATTTAAGAGATTCTCCCAGGATCACAGTTAGGTAACAGAGCTGGAT AGAATATTAGGATTCAGAGATATTAAGAGATTCTCCCAGGATCACAGTTAGGTAACAGAGCTGGAT AGAATATTAGGATTCAGAGATATTAAGAGATTCTCCCAGGATCACAGTTAGGTAACAGAGCTGGAT AACGTATATACACCCTTTGTATAACATGTCACGAATTCAGCATAAAGGGATCTTCAGTGATCTAA AACGTATATACACCCTTTGTATAACATGTCACGAATTCAGCATAAAGGGATCTTCAGTGATCTAA AAAGGACCAAATAGTAATATTCAGGCTTTGTGAGATTCAGCATAAAGGGGATCTTCAGAATCTAA AAAGGACCAAATAGTAATATTCAGGCTTTGTGGACCCTATGGTCTTATCATAACTGTTCAAATC AAAGGACCAAATAGTAATATTCAGGCTTTGTGGACCCTATGGTCTTATCATAACTGTTCAAATC AAAGGACCAAATAGTAATATTTCAGGCTTTGTGGACCTATGGTCTTATCATAACTGTTCAAAAC AAAGGACCAAATAGTAATATTTCAGGCTTTGTGGACCTATGGTCTTATCATAACTGTTCAAAAC AAAGGACCAAATAGTAATATTTCAGGCTTTTGTGGTCTTTAATAACTGTTCAAAAA AAAGGACCAAATAATATTTCAGGCTTTTTTAAGGGATTTTTAACTGTTTAAAAAAAA		(1457) 1457	1470	1480	1490	1500	1510	1520	1530	1547
CAGAGATATTAAGAGATTCTCCCAGGATCACAGITAGGIAACAGAGCTGGATTTTAGICCAG CAGAGATATTAAGAGATTCTCCCAGGATCACAGITAGGIAACAGAGCTGGATTTTAGICCAG CAGAGATATTAAGAGATTCTCCCAGGATCACAGITAGGIAACAGAGCTGGATTTTAGICCAG Section 1680 1600 1700 1710 1680 1710 Section 1700 1710 Section 1680 1700 1700 1700 1700 1700 1700 1700 17	ID NO 6(1457)	TCTTTT62	AAAGAGAATA: 		BGATATTAAC	SAGATICICO	CASGATCACA	GITAGGIAAC	AGAGCTGGATT	TTAGICCAGG
CAGAGAIATIAAGAGAITCICCCAGGAICACAGITAGGIAACAGAGCIGGAITTIAGICCAG 1580 1580 1600 1610 1620 CCITTGTATAACATGICACGAATTCAGCATCATCAGTGATCTAAGTCAGGGGTC	NO 16(1152)	TCTTTTE	AABGAGAATA:	0.0000000	BGATATTABE	SAGATICICO	CAGGATCACA	GITAGGIAAC	AGAGCTGGATT	TTAGTCCAGG
1580 1690 1600 1620 1710	nsensus(1457)	LCTTTTGF	AAAGAGAATA		AGATATTAAG	AGATTCTCC	CAGGATCACA	GTTAGGTAAC	AGAGCTGGATT	TTAGTCCAGG
CCITTGTATAACAISICACGAAITCAGCATAAAGGGAICITCAGTGAICIAAGTCAGGGGIC	(1548)			1570	1580	1590	1600	1610	1620	7-
CCITIGIAIAACAIGICACGAAIICAGCAIAAAGGGAICIICAGIGAICIAAGICAGGGGIC CCITIGIAIAACAIGICACGAAIICAGCAIAAAGGGAICIICAGIGAICIAAGICAGGGGIC Sedic 1670 1680 1690 1700 1710 TAATAIIICAGGCIIIGIGGACCCIAIGGICICIAICAIAACIGIICAAAICACCAIGIAGI TAATAIIICAGGCIIIGIGGACCCIAIGGICICIAICAIAACIGIICAAAICACCAIGIAGI TAATAIIICAGGCIIIGIGGACCCIAIGGICICIAICAIAACIGIICAAAICACCAIGIAGI TAATAIIICAGGCIIIGIGGACCCIAIGGICICIAICAIAACIGIICAAAICACCAIGIAGI AATAITICAGGCIIIGIGGACCCIAIGGICICIAICAIAACIGIICAAAICACCAIGIAGI Sectic TAACGAATGIGGCICIIITAIAGGGAIIIITIIITAACICIIIACAAAAAAAAAGCAGGCCA	ID NO 6(1548)	TGICIACAS	SCICIAACGI	ATATACACCCI	TEGEATABEE	TETCACGAR	ITCAGCATAA	AGGGATOITC.	AGIGAICIAAG	TCAGGGGTCA
1670 1680 1690 1700 1710	0 NO 16 (1243) 0 NO 16(1243) nsensus(1548)	TGTCTACAC	SCICIAACGIA	100	TTGTATAAC!	ATGTCACGAA	TCAGCATAA TTCAGCATAA	AGGGATCTTC. AGGGATCTTC.	 AGTGATCTAAG AGTGATCTAAG	TCASSSSTCA TCAGGGGTCA TCAGGGGTCA
TAATATITCAGGCITIGIGGACCCIAIGGICTCTAICAIAACIGITCAAAICACCAIGIAGT TAATATITCAGGCITIGIGGACCCIAIGGICTCTAICAIAACIGITCAAAICACCAIGIAGT Section 1760 1770 1780 1790 1800 1810 TAACGAATGIGGCIGITITAIGGGATIIIIITIAACICIIITAIIIACAAAAGCAGGIGGCA	(1639) ID NO 6(1639)	1639 AACCITITC	1650 TAAAAAGGA!	1660 SCAAAIAGIAA	1670 TATITCAGEC	1680 TITGIGGAC	1690 CCTATGGICT	1700 CIATCATAAS	1710 TSIICAAAICA	3350
0 1750 1760 1770 1780 1790 1800 1810 agcaaaatataaactaacgaatgtgsststttatgssatitttaactsttacaaaagsasssa	NO 16(1334)	AACCIITIC	TABABAGGAGTA		TATTTCAGGC	TTTGTGGAC	CCIAIGGICT	CTATCATAAC	TGTTCAAATCA IGTTCAAATCA	CCATGIAGIG
AGCAAAATATAAAC	(1730)	1730	1740	1750	1760	1770	1780	1790	1800	
	ID NO 6(1730)	AAAGGAGOC	SATABGCAAAA	ATATAAACTAA	CGAATGTGGC	STETTIBLE	COMPTETITE	TTAACTOTIT	ATTIACAAAAG	DAGGTGGAG

SEQ ID NO 6(1821) CAGAACTCACTTATGGGCCATAGTTCTCTGACCCTGAGGAAATCTTATATGGACAACTTTAGACTGTGACTTGCCAAGTA	CCATAGITCIC CCATAGITCIC CCATAGITCIC CAACTGAAGGI CAACTGAAGGI CAACTGAAGGI CAACTGAAGGI CAACTGAAGGI AACTGAAGGI	CTGACCCCTG CTGACCCCTG CTGACCCCTG TCAAGGCTGG TCAAGGCTGG TCAAGGCTGG	ACCTGAGAA ACCTGAGAA ACCTGAGAA 1950 AGTTCTGAA AGTTCTGAA AGTTCTGAA	AATCTIAIA AATCTIAIA AATCTIAIA AGCAAAGAG AGCAAAGAG AGCAAAGAG	CCCCTGACCIGAGAAATCTTAIAITTAIGGACAACATTIAGACTGTGACTTGCCAAGTA	ACATTIAGA ACATTIAGA ACATTIAGA TTAATGATA TTAATGATA	CTGTGACITG CTGTGACITG CTGTGACITG AGTGAAATAG AGTGAAATAG AGTGAAATAG	
CONSENSUS (1516) CAGAACICACITATGGGC CONSENSUS (1821) CAGAACICACITATGGGC CONSENSUS (1822) 1920 EQ ID NO 6(1912) AGAACAAGAAGCTCTGTC CONSENSUS (1912) AGAACAAGAAGCTCTGTC CONSENSUS (1912) AGAACAAGAAGCTCTGTC CONSENSUS (1912) AGAACAAGAAGCTCTGTC COND NO 6(2003) 2003 2010 2010 2010 13 (306)	CATAGITCTC CATAGITCTC 1930 AACTGAAGGI AACTGAAGGI AACTGAAGGI AACTGAAGGI	TGACCCCTG TGACCCCTG 1940 CAAGGCTGG CAAGGCTGG CAAGGCTGG	ACCIGAGAA ACCIGAGAA 1950 AGITCTGAA AGITCIGAA	AATCTTATA AATCTTATA 1960 AGCAAAGAG AGCAAAGAG AGCAAAGAG	ATTIAIGGACA ATTIAIGGACA 1970 CIGICIGGIC COTGICIGGIG	ACAITIAGA ACAITIAGA 1980 HIAALGATA TIAATGATA TIAATGATA	CTGTGACITG CTGTGACITG 1990 AGIGAAATAG AGTGAAATAG	CCAAGIA CCAAGIA -Section 22 2002 TIAAAAGI -ITAAAAGT TITAAAAGT
Consensus(1821) CAGAACTCACTTATGGGC (1912) 1912 1920 EQ ID NO 6(1912) AGAACAAGAAGCTCTGTC Q ID NO 13 (306) Consensus(1912) AGAACAAGAAGCTCTGTC Consensus(1912) AGAACAAGAAGCTCTGTC CONSENSUS(1912) AGAACAAGAAGCTCTGTC CONSENSUS(1912) AGAACAAGAAGCTCTGTC Q ID NO 6(2003) TAGAAGATCCCAGTTATA Q ID NO 13 (306)	CATAGIICIC 1930 AACIGAAGGI AACIGAAGGI AACIGAAGGI AACIGAAGGI	1940 1940 1946 1946 1946 1946 1946 1949	ACCIGAGAA 1950 AGITCTGAA AGITCTGAA AGITCTGAA 2040	AATCTTATA 1960 AGCAAAGAG AGCAAAGAG AGCAAAGAG	1970 1970 SCIGICIGGIS SCIGICIGGIG	ACATITAGA 1980 ITAAIGATA ITAAIGATA	1990 AGIGAAATAG AGIGAAATAG AGIGAAATAG	CCCAAGTA -Section 22 2002 TTAAAGT TTAAAGT TTAAAGT TTAAAGT
(1912) 1912 1920 EQ ID NO 6(1912) AGAACAAGAAGCTCTGTC Q ID NO 13 (306)	1930 AACTGAAGGT AACTGAAGGT AACTGAAGGT AACTGAAGGT	1940 CAAGGCTGG CAAGGCTGG CAAGGCTGG	1950 AGIICTGAA AGIICTGAA AGIICTGAA 2040	1960 AGCAAAGAG AGCAAAGAG AGCAAAGAGAGAGAGAGAG	1970 CIGICTGGIC CIGICTGGIG	1980 IITAAIGATA IITAAIGATA ITTAAIGATA	1990 AGIGAAATAG AGIGAAATAG AGIGAAATAG	2002 TEAAAGI TIAAAGI TTAAAGI
EQ ID NO 6(1912) AGRACAAGAAGCTCTGTC Q ID NO 13 (306) Q ID NO 16(1607) AGAACAAGAAGCTGTGTC Consensus(1912) AGAACAAGAAGCTCTGTC Consensus(1912) AGAACAAGAAGCTCTGTC (2003) 2003	AACTGAAGGT AACTGAAGGT AACTGAAGGT AACTGAAGGT	CAAGGCTGG CAAGGCTGG CAAGGCTGG	AGITCTGAA AGITCTGAA AGITCTGAA 2040	ACCAAACAG AGCAAAGAG AGCAAAGAGAGAGAGAGAGA	CIGICIGGIC	TTARIGATA TTARIGATA TTARIGATA	AGIGAAATAG AGIGAAATAG AGIGAAATAG	TIBARGI TIBARGI TIBARGI TIBARGI -Section 23
O ID NO 16 (1607) AGAACAAGAAGCTCTGTC Consensus(1912) AGAACAAGAAGCTCTGTC Consensus(1912) AGAACAAGAAGCTCTGTC (2003) 2003	AACTGAAGGT AACTGAAGGT 20 20	CAAGGCIGG CAAGGCIGG 030	AGTICTGAA AGTICTGAA 2040	AGCAAAGAG AGCAAAGAG 2050	CIGICIGGIG	TIAAIGAIA	AGTGAAATAG AGTGAAATAG	TIAAAGT TIAAAGT - Section 23
2010 (2003) 2003 2010 20 EQ ID NO 6(2003) TAGAAGATCCCAGTTATA Q ID NO 13 (306)	20 20 8 GAAGCACAA	030	2040	2050	0900	000	000	6006
EQ ID NO 6(2003) TAGAASATCCCAGTTATA Q ID NO 13 (306)	AGAAGCACAA				2007	20/0	2080	2020
		agaataatg 	ACCATAGAC	TCCIGAACA	ATAATGACCATAGACICCIGAACAAGAAIGICIGGACIICTGGCTIAGGCACICIIGIIG	GACTECEG	CTIRGGORUI	CITGITG
SEQ ID NO 16(1698) TAGAAGATOCCAGTTATAAGAAGGACAAAGA Consensus(2003) TAGAAGATCCCAGTTATAAGAAGCACAAAGA	RGAAGCACAA AGAAGCACAA	AGAATAATG AGAATAATG	ACCATAGAC ACCATAGAC	TCCTGAACA TCCTGAACA	ATAATGACCATAGACTCCTGAACAAGAATGTCTGGACTTCTGGCTTAGGCACTCTTGTTG ATAATGACCATAGACTCCTGAACAAGAATGTCTGGACTTCTGGCTTAGGCACTCTTGTTG Section 24	GACTICIEG	CITAGGCACI	CTTGTTG CTTGTTG
(2094) 2094 2100 2110	0 2120		2130	2140	2150	2160	2170	2184
SEQ ID NO 6(2094) TATGGTCCAGGCCAAGTTACCTAATCTCTCCAGGCCTCCATTTTCTTAATGAAGATAATAAAAGATTTTTCCTCAGAGAGAG	ACCIAAICIC	TCCAGGCCT	CCATITICI	TAICATIAA	ATGAAGATAA	TARAAGIAT	ITICCICAGA	GAGCTGT

2260	TGCCAG	TOCCAG	TGCCAG
2250	TCAATAAA		ATCAATAAA
2240	TATIAATIT	 FATIAATIF?	TATTAATT1
2200 2210 2220 2230 2240	A OCTA A CCCATGT CAA GCA CATAGAATA GGGCCCAGCCTATATTAATTTATCAATAATGCCAG		SGCCCAGCCIA
2220	CATAGAATAG	 CATAGAATAGO	CATAGAATAGG
2210	TGTCAAGCA	 TGTCAAGCACATA	TGTCAAGCA
2200	reascraaccea		IGAGCTAACCCA
2190	ATAAACI	ATAAACI	ATAAACI
(2185) 2185 2190	SEQ ID NO 6(2185) AAGAATAAGTGA	SEQ ID NO 13 (306)	Consensus(2185) AAGAATAAACTGAGCTAACCCATGTCAAGCACATAGAATAGGGCCCCAGCCTATATTAATTTAATTAA

EXHIBIT E

SEQ NO 13, 15 and 16 against SEQ NO 7

	(1) 1	10	50	30	40	20	90	70	80	91
SEQ ID NO 7 SEQ ID NO 13		# # B	AACTTAGTAA AACTTAGTAA	ABOCAGACGC ABGCAGACGGC	CAGACGGCTCTCACCAATAAGGGCAGGCA CAGACGGCTCTCACCAATAAGGGCAGGCA	AAGGGCAGGC AAGGGCAGGC	S 3	TGTCGAAAC TGTCGAAAC	CATCCAATCTGTCGAAAGCTTGAATAAAAAAAG CATCCAATCTGTCGAAAGCTTGAATAAAAAAA	ACAAAAG Acaaaaag
SEQ ID NO 16 Consensus		 	 		TCTCACCAAT		TCATC	TGTCGAAAG	CITGAATAAA	 ACAAAAG Section 2
SEQ ID NO 7 SEQ ID NO 13 SEQ ID NO 15		(92) 92 100 110 (92) AGGAASGSAAAAITTGCTTCTTTC (92) AGGAAGGGAAAATTTGCTTCTTTTC (1)	110 FTGCTTCTTT	[120 130 140 ITCTTGATCTAGTATATCATCTTCTCCTGC ITCTTGATCTAGTATATCATCTTCTCCTGC	140 AICTICICO AICTICICO	150 GCCCITGGAT	160 STGAGTGGGC STGAGTGGGC	150 170 180 180 170 182 CCITGGATGISAGGGCCITCAGACTIAAACCAGG	182 482 482 482 482 483 483 483 483 483 483 483 483 483 483
SEQ ID NO 16 Consensus		(1)(1) AGGAAGGAAAATITGCTTCTTT	TIGCTICTII	 TCTTCTTGA	 TCTAGTATATC	CATCTTCTCC	CCIGCCCIIGGAIO	STGAGTGGGC	TGGATGTGAGTGGGCCTTCAGACTT	TAAACCAGG
	(183) 183	190	200	210	220	230	240	250	260	273
SEQ ID NO 7 SEQ ID NO 13 SEQ ID NO 15	7 (183) AGT 3 (183) AGT 5 (1)	SEQ ID NO 7 (183) AGTTACACCTTTGGCTTCCCTGGTT SEQ ID NO 13 (183) AGTTACACCTTTGGCTTCCCTGGTT SEQ ID NO 15 (1)	SCTTCCCTGC SCTTCCCTGC	STICTCAGITC	CITTGGACTIG CITTGGACITG	GACTGAATT/ GACTGAATT/ 	OTCAGTICTITGGACTIGGACTGAATTACACTGCCAGGTITCCTGGTTCTCCAGGTIGGC CTCAGTICTITGGACTIGGACTGAATTACACTGCCAGGTITCCTGGTTCTCCAGACTTGCAGATGGC 	TTTCCTGGT3 TTTCCTGGT3	CICCAGCIIG CICCAGCIIG	TGCAGATGGC TGCAGATGGC
SEQ ID NO 16 Consensus	(183) AGTI	Consensus (183) AGTTACACCTTTGGCTTCCCTGG	CTTCCCTGG	TICICAGII	CTTTGGACTTG	GGACTGAATTA	TACACIGCCAGGT	TTCCTGGTT	CTCCAGCTTGCAGATGGC	CAGATGGC Section 4
	(274) 274	280	290	300	310	320	330	340	350	364
SEQ ID NO 7 SEQ ID NO 13	7 (274) AGA 3 8 (274) AGA 3	CATGGGA	CTIGGCCIC	TAATIGI	TAATIGIGGCCAAAAGGAAAGAAAAAAAAAAAAAAAAAAA	AAAGAGACAA	AACAGCATGAAATGAT	AATGATGAGAC	CCAAGTSATGAAAAT	8 - 6 - 6 - 6 - 6 - 6 - 6 - 6 - 6 - 6 -
SEQ ID NO 16	(E) (E)								9 - K	5
Consensus	(274) AGAI	Consensus (274) AGAICAIGGGACTICTIGGCCICCA	CIIGGCCIC	\vdash	GGCAAAAAGG	AAAGAGACA?	AATTGTGGGCAAAAAGGAAAGAGACAAAACAGCATGAAATGATGAGACCAAGTGATGAAATTCA	AATGATGAGA	CCAAGTGATG	AAAATTCA

SEQ NO 13, 15 and 16 against SEQ NO 7

SEQ DNO 17 (365) TEACAATGATIFCCTTCCAAGGATATITCCTTGGGTAATTCAGGGGCCTGTTACTATGGGGGGGGGG		(365) 365	370	380	390	400	410	420	430	440	455
SECIDINO 16 (60) TICACAATGAITGCITICAAGAGIAATITCICITGGGTAATTCAGCGGCCTGTAATGGCGAGGGTGAATGGTAAATGAA SECIDINO 16 (1)	Q ID NO 7	7 (365) TTC 3 (306)	ACAATGAT 	TGCTTTCA	6-1	CICITGEGIA	ATTCAGCAGC	Cretiacial	GGCTCTGG	AGTGATAGCTA	ATGIABAIGAA
Consensus (365) TICACAATGATTGCTTTCAAGGGTAATTGCTGTGGGTAATTGCTGTGGGTTTACTGTGGGTGG	ID NO 15	5 (60) TTC	ACARTGAT	TGCTITCA	£	CICIIGGGIF	ATTCAGCAGC	CIGILACTAT	eechcrores.	AGTGATAGCTA	AIGIAAAIGAA
470 480 480 500 500 510 520 530 SICTABABAGIGGATIATICCIGACAAGAATATACICAGCCAATAATGCAACAGAAATCCATTCAAAGCATTCGGGAAAAATTCAAAAG SICTAAAAGTGGATTATCCIGACAAGAATATACICAGCCAATAATGCAACAGAAATCCATTCAAAGCATTCGGGAAAAATTCAAAAG SICTAAAAGTGGATTATTCTGACAAGAATATACICAGCCAATAATGCAACAGAAATCCATTCAAAGCATTCGGGAAAAATTCAAAAG SATATCTTTTTTTTTTAAAGTTAATGACCTACGATCCATTCTTCCTCGACTAACAAGCACTTAAAAATTCCAGC AATATCTTTTTTTTTT	Consensus	(1) === (1) (365) (1) (1) (1) (1)	ACAATGAT	TGCTTTCA	◘	CICIIGGGIA	ATTCAGCAGC	CIGITACIAI	GGCICICIGG	AGTGATAGCTA	ATGTAAATGAA Section 6
O D O (456) GCCCCTABABAGTGGGATTATCCTGACABATATACCAGCCAATAATGCAACAGAAATCCAATCC		(456) 456		470	480	490	200	510	520	530	546
NO 15 15 15 15 15 15 15 1	EQ ID NO 7	7 (456) GCC 3 (306)	TCTAAAAG	TGGATTAT(TETERCARGA	ATATACICAG	CARTARIGO	AACAGAAAIC	CATTCAAAGC	AIICGGGAAAA	AIICAAAAGAA
Section	D 00 15	5 (151) GCC	TCIAAAAG	TGGATIAIC	CICACAGA	ATATACICAC	CAATAATGO	AACAGAAATC	CATTCAAAGC	ATTCGGGAAAA	ATTCARARGAR
580 590 600 610 620	Consensus	(1) (456) GCC	TCTAAAAG	TGGATTATC	CTGACAAGA	 ATATACTCAG	CCAATAATGC	AACAGAAATC	 CATTCAAAGC	 ATTCGGGAAAA	
TAATGACCIACGATCCATTICITCCCTGACTAACAAGCCAAGC		(547) 547		560	570	280	290	009	610	620	637
TAATGACCIACGATCCATTICITCCCTGACTAAGAGCAGCAAGCACTTAAAAATATCCAGC TAATGACCTACGATCCATTICITCCCTGACTAAGCAGCAAGCACATTAAAAATATCCAGC Section	O ID NO 7	7 (547) TRA	RIBIECII	TITITITI	FITAAAGITA	ATGACCIAC	ATCCATTICI	TCCCTGACTA	ACAAGCAGCA	AGCACTTARAA	ATATCCAGCCA
TAATGACCTACGATCTTCCTGACTAACAAGCAGCAAGCACTTAAAATATCCAGC	ID NO 15	5 (242) TAB		TITITI	 CITAAAGITA	ATGACCIACO	SAICCATITUT	TCCCTGACTA	ACAAGCAGCA	 agcactiabab	# 1 # 1 C C A C C C A
570 580 690 700 710 11.0 12.0 13.0	Oonsensus	5 (1) 5 (547) TAA.	ATATTCTT	 T T T T	TTAAAGT	 ATGACCTACG	 CATTT	TCCCTGACTA	acaacaaca	 agcacttaaaa	ATATCCAGCCA
		(638) 638		650	099	670	089	069	700	710	728
	OID NO 7	7 (638) GGA	TSAAATAG	AAACCCACC	TISHCITGLI	TELLET	TIT	GGGACICAGA	TICTAAGCCA	TICILE	\mathcal{C}
(1)	U NO 15	333) GGA 333) GGA	 TGAAATAG	AAACCCAC	1 5-3	I		1 (5-)	TTCTAAGCCA		TGATOTIGGCA
	Onsensus	. (438) GGB					1 E		A C C C A A E C E E		

SEQ NO 13, 15 and 16 against SEQ NO 7 $\,$

819	TAAAACCTTT TAAAACCTTT 	AACCTTT - Section 10 910		1001	TCAGGT TCAGGT TCAGGT	Section 12	7801
	TAGITITAAAAACCIIT 	GTTTTAAAA 900 TGGCATTI	TGGCATTC	066	TCCTGSGCGTTTCAGGT 	0000	CCCACCAT
800	AMATICATIA AMATICATIA AMATICATIA	AAATIGATIA 890 ISGSICAGGI	 !::::::::::::::::::::::::::::::::	980	SCAGCAGITC	40.70	100 P C P C P C P C P C P C P C P C P C P
790	CAIGAAIGGGIGTCAAAATIGAT 	ATGGGTGTCAA 880 SCCTTTCAT	GCCTTTCAT	970	AGAATCTGGGCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	000	CACCCTGTGTGCATGACAGG
780	CITIATCITGGAAAAAGTITCAIGAAIGGGTGTCAAAATIGATIAGITI 	TITICITTATCTIGGAAAAAAGITICAIGAATGGGIGICAAAATIGAITAGITTIAAAAACCITI Section 10 850 860 870 880 890 900 AACTGIAITASAAAAAATIICAIAICICCASGCCITICATISGSICAGGITGGCAITICGCIGCC		096	AAGGAAAGAAAAACICAAGIGAAGAAAATUAGAAICIGGGGAGCAGTICUGGGGGGTT	4060	
770	TTCTTTATCTTGGAAAAAAGTTT 	TIGGAAAAAA 860		950	AAACTCAAG 	0.7	
760	TITCITIALC TITCITIALC	TITCITIAIC 850 ACTGIAITAS	ACTGTATTAGA	940	1006886888 	0000	AGCCCAGCATCCATCT
750	348 348	TIGCCAACTI 840	CACCCTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	930	GICAAAAIAA 	0000	CCTCATCAAC
740	SEQ ID NO 7 (729) AATGTCTCGAATTATTTTTGCCAAC SEQ ID NO 13 (306)	Consensus (729) AATGICICGAATTATTITGCCAAC (820) 820 830 840 SEQ ID NO 7 (820) CITSCAGAIACGIAIGGCACCTAA	SEQ ID NO 13 (306)	920	SEQ ID NO 7 (911) CITIAICS CSTGAGGGGGAAAN EQ ID NO 13 (306)	C	SEQ ID NO 7(1002) GCTTCCCACATCACCTGCCTCATCA SEQ ID NO 13 (306)
(729) 729	(729) AATGICI (306) (424) AATGICI (1)	(729) AATGTCT (820) 820 (820) CTIBCAG	(306) (515) CTTSCAS (1)	(911) 911	(911) CRITARIOR (306) (558) (49) CRITARGT (911) CRITARGT	0007	(1002) FORE (1002) GCTICCCA (306) (558) (140) GCTICCCA
	SEQ ID NO 7 (729) AAT SEQ ID NO 13 (306) SEQ ID NO 15 (424) AAT SEQ ID NO 16 (1)	Consensus (SEQ ID NO 13 (SEQ ID NO 15 (SEQ ID NO 16 Consensus (SEQ ID NO 7 (911) CTT SEQ ID NO 13 (306) SEQ ID NO 15 (558) SEQ ID NO 16 (49) CTT Consensus (911) CTT		SEQ ID NO 7(1002) 1002 SEQ ID NO 7(1002) GCTT SEQ ID NO 13 (306) SEQ ID NO 15 (558)

SEQ NO 13, 15 and 16 against SEQ NO 7 $\,$

TCACCCCCCTACTTAGCCAGATATACAAGAATATCTGCACGGATGACCTGCCTCACCT TCACCCCCCTACTTAGCCAGATATACAAGAATATCTGCACGGATGACCTGCCTCACCT TCACCCCCCTACTTAGCCAGATATACAAGAATATCTGCACGGATGACCTGCCTCACCT TCACCCCCCTACTTAGCCAGATATACAAGAATATCTGCACGGATGACCTGCCTCACCT TCACCCCCCTACTTAGCCAGATATACAAGAATATCTGCACGGATGACCTGCCTCACCT TCACCCCCCTACTTAGCCAGATATACAAGAATATCTGCACGGATGACCTGCCTCACCT TCACCCCCCTACTTAGCCAGATATACAAGAATATGCCCCCAAAAT TSO TSO TSO TSO TSO TSO TSO	77(1093) TCAGAGCAAAG 13 (306) 15 (558) 16 (231) TCAGAGCAAAG sus(1093) TCAGAGGCAAAGG		-	7		-		1170	1102
AAGGCICTCCCACTATICIGGITCACCCCCTACTIAGCCAGATATACAAGAATATCIGCACGGAIGACCIGCCICACCT AAGGCICTCCCACTATICIGGITCACCCCCCTACTIAGCCAGATATACAAGAATATCIGCACGGAIGACCIGCCICACCT Bedio 1200 1200 1210 1220 1220 1230 1240 1250 1260 1260 1260 1260 1260 1260 1260 126	13 (306)	SCICICCCAC	TATTCTGGTT	CACCCCCCTAC	TTAGCCAGAT	ξ. Σ.	TCTGCACGG	4 T GACCTGCCTC	CACCIGGG
AAGGCTCTCCCACTATICIGGTTCACCCCCTACTTAGCCAGATATACAAGAATATCIGCACGGATGACCTGCCTCACCT AAGGCTCTCCCACTATICIGGTTCACCCCCCTACTTAGCCAGATATACAAGAATTCTGCACGGATGACCTGCCTCACCT Section 1200	16 (231) ICAGAGCAAAGO sus(1093) ICAGAGCAAAGO		 						
AAGGCTCTCCCACTATTCTGGTTCACCCCCTACTTAGCCAGATATACAAGAATATCTGCACGGATGACCTGCCTCACCT Section 120 120 120 120 120 120 120 120 120 12	sus(1093) TCAGAGCAAAG	SCICICCCAC	():	24	TIAGCCAGAT	ATACAAGAATA	rerecaded	ATGACCIGCCI	SACCIGGG
1200 1200 1210 1220 1230 1240 1250 1260		SCICICCCAC	ICI	CACCCCCTAC	TTAGCCAGAT	ATACAAGAATA	TCTGCACGG	ATGACCIGCCIC	CACCTGGG — Section 14
GGRGCTCAGATICCAITACIAICGCACCAAGGATCTCCCAGCAAGAAIGACAGAAAGACIAACTGCCCCCAAAAT GGAGCTCAGATICCAITACIAICGCACCAAGGATCTCCCAGCAAGAAIGACAGAAACTGCCCCCCAAAAT GGAGCTCAGATTCCAITACIAICGCACCAAGGATCTCCCAGCAAGAAIGACAGAAACTGCCCCCCAAAAT GGAGCTCAGATTCCAITACIAICGCACCAAGAATGTGCCTCCAGCAAGAAAGACTAACTGCCCCCCAAAAT AACACAGTTCTCTTAATTCTCCCAAGAAACCAGAATGTGACTGCTCACCTCTTAAGGACCTGAAAACAACTGGCCATTT AACACAGTTCTCTTAATTCTCCCAAGAAACCAGAATGTGACTGCTCACCTCTTAAGGACCTGAAAACAACTGGCCATTT AACACAGTTCTCTTAATTCTCCCAAGAAACCAGAATGTGACTGCTCACCTCTTAAGGACCTGAAAACAACTGGCCATTT AACACAGTTCTTTAATTCTCCCAAGAAACCAGAATGTGACTGCTCACCTCTCTAAGGACCTGAAAACAGACTGGCCATTT AACACACAGTTCTTTAATTCTCCCAAGAAACCAGAATGTGACTGGTTGGT	(1184) 1184 1190	1200	1210	1220	1230	1240	1250	1260	1274
GGAGCTCAGATICCAITACIATCGCACCAAGGACAGATCTCCCAGCAAGAATGACAGAAAAGACTAACTGCCCCCAAAATGGGACCCCAAAATGGGACCAGATCTCCCAGCAAGAATGACAGACTAACTGCCCCCCAAAATGGGACCTCAGTTCCCATACTGCCCCCCAAAATATACAACTTCCTTAATTCTCCCAAGAAACAACTGTGACTGCTCACTCTCTAAGGACCTGAAAACAACTGGCCATTTAACAACAGTTCTCCTAAGAACAAAAAAAA) 7(1184) AGCTCAGAGGA(13 (306)	SCTCAGATIC	CATTACTATC	3CACCAAGGAC	AGATOTOCOA	GCAAGAATGAC 	AGAAAABA 	182CTGCCCC	18882CIC
AGCICAGAGGAGCICAGATICCAITACIAICGCACCAAGGAICTCCCAGCAAGAAIGACAGAAAAGACTCCCCAAAAI AGCICAGAGGAGCICAGATICCAITACIAICGCACCAAGGAICTCCCAGCAAGAAIGACAGAAAAAGACTACTGCCCCCAAAAI Sectio 1275 1280 1290 1300 1310 1320 1330 1340 1350 CCTICCAAAACAACAGTICTCTCCCAAGAAACCAGAAIGTGACTGCTCACCTCTAAGGACCTGAAAACAACTGGCCATIT CCTICCAAAACAACAGTICTCTIAAITCICCCAAGAAACCAGAAIGTGACTGCTCACCTCTTAAGGACCTGAAAACAACTGGCCATIT CCTICCAAAACACAGTICTCTIAAITCICCCAAGAAACCAGAAIGTGACTGCTCACCTCTTAAGGACCTGAAAACAACTGGCCATITCCTTTAAAACAACAGTTCTCTTAAAACAACAAAATCAAAAAATCAAAAAATCAAAAAA	- 1							Ĺ	
AGCTCAGAGGAGCTCAGATTCCATTACTATCGCACCAAGGACAGCAAGAATGACAAGAATGACAGAAAAGACTAACTGCCCCCAAAAT	16 (322) AGGTCAGAGGA	SCICAGAFIC	SATTACTATO	CORCORROGRO	AGAICICCCA	GCAAGAATGAC	AGARARGAC	SAACTGCCCCC	SABARCEC
1280 1290 1300 1310 1320 1330 1340 1350	.us(1184) AGCTCAGAGGA(SCICAGAIICO	A	GCACCAAGGAC	AGATCTCCCA	GCAAGAATGAC	AGAAAAGAC	IAACIGCCCCC	AAAATCTC — Section 15
CCTICCAAAACACTICICITAAITCTCCCAAGAAACCAGAAIGTGACTGCICACCTCTAAGGACCIGAAAACAACTGGCCATIT	(1275) 1275 1280	1290	1300	1310	1320	1330	1340	1350	1365
CCTTCCAAAACACAGTTCTCTTAATTCTCCCAAGAAACCAGAATGTGACTGCTCACCTCTTTAAGGACCTGAAAACAACTGGCCATTT CCTTCCAAAACACAGTTCTCTTAATTCTCCCAAGAAACCAGAATGTGACTGCTCACCTCTCTAAGGACCTGAAAACAACTGGCCATTT Section 1380 1400 1410 1420 1430 1440 CTAITTAAATCAACTTTAAAAAAATCCAACCGCCAAAATATTAAACCATTTTGGTTGG	O 7(1275) CCTTCCAAAACA	SCAGTICICI	DDDLDLIEWJ	AAGAAACCAGA	ATGIGACIGO	TOMOCICICIE	AGGACCIGA	ABACBACTGGGG	DATE TO AG
CICCCAAGAAACCAGAAIGIGACIGCICACCICICTAAGGACCIGAAAACAACIGGCCAITI TCICCCAAGAAACAGAAIGIGACIGCICACCICICTAAGGACCIGAAAACAACIGGCCAITI Section	13 (306) 15 (558)	1 1	1 1			1 1			
TCTCCCAAGAAACCAGAATGTGACTGCTCACCTCTAAGGACCTGAAAACAACTGGCCATTT	16 (413) CCTTCCAAAC	SCAGITCICI	TARTICICC.	AAGAACCAGA	ATGTGACISC	TOIDO	ROHOUMOUR	AAACAACIGGC	ATTICAG
990 1400 1410 1420 1430 1440 CAACCGCCAAAAIAIIAAACCAIIIIGGIISGAAIGAIAACAIAAC	sus(1275) CCTTCCAAACA	ACAGIICICI	\vdash	AAGAAACCAGA	ATGTGACTGC	TCACCICICIA	AGGACCTGA	AAACAACIGGC	SATITCAG Section 16
CAACCGCCAAAAIAITAAACCATITIGGTIGGAAIGATAACAIAACIAACCIGCIGACAGC 	(1366) 1366	1380	1390	1400	1410	1420	1430	1440	1456
	O7(1366) CTAITIAAAIC	ARCITIABAA		CARARAIRIT	AACCATI	GIIGGAAIGAI	AACATAACI	AACCTGCTGAC	(.) (t)
OB A COGOGRABATA TER A ROCA TITISGETISGA BIGATARCATARCIA BOCTAR COTIGA CA	 								
	16 (504) CRATTIABATC)	SACTTIBABA	A A T C C A A C C G	CCAAAATATTA	AACCATITIE	GTIGGAAIGAT	AACATAACT	AACCIGCIGAC	TIDETOS

SEQ ID NO 7 (1457) CTGCTAGGTGGAAAAATGGAAAAAAATACTICTAATCAGGTGAAATCACTCTACCTTTGGGATCTAAATTTACTCAAAGA SEC ID NO 16 (568) SEC ID NO 16 (568) SEC ID NO 16 (568) CONSENSUS (1458) ISSUED A STATEMENT OF THE CONTROL OF THE C	AATACTTCTAATCAGGTCAAATCACTCTAGGGATTCTAAATTTACTCATA AATACTTCTAATCAGGTCAAATCACTCTACCTTTGGGATTCTAAATTTACTCATA AATACTTCTAATCAGGTCAAATCACTCTACCTTTGGGATTCTAAATTTACTCATA AATACTTCTAATCAGGTCAAATCACTCTACCTTTGGGATTCTTAAATTTACTCATA TAGGATTATTCCTTTAGCTCGATAAGCAACCAGAAGTTCTTCCTTC	(1457) 1457	1470	1480	1490	1500	1510	1520	1530	1547
IGCAAAAAIGGAAAAAAAAAAAAAAAAAAAAAAAAAAAA	AATACTICTAAICAGGICAAATCACTCTACCTITGGGATTCTAAATTTACTCATA 1580	SEQ ID NO 7(1457) CTGCTAG SEQ ID NO 13 (306) SEQ ID NO 15 (558)	OTGCAAAAATG 		PACTICIAAT:	ZAGGTCAAAT	0 A C T C T A C C C C C C C C C C C C C C	TTTGGGATTC	TAAATITACICAL	ATTCTCABAG
1580 1590 1600 1610 1620 1720 1730 1730 1730 1730 18310 1730 1730 1730 18310 1730 1730 18310 1730 1730 18310 1730 1730 18310 1730 17	1560	16 (595) CIGCIAS sus(1457) CIGCIAG	GTGCAAAAATG GTGCAAAAATG	GAAAAAAAA GAAAAAAAA	RACTICIAAT RACTICIAAIO	CAGGTCAAAT	CACTCTACC	TITGGGATIC TITGGGAIIC	TABATTTACTCAT. TAAATTTACTCAT	ATICICAAAG ATICICAAAG
CAGTCATAGTGGGGAAAATAGGATTAITCCITIAGCICGATAAGCAACCAGAAGTICTICCTICAAATCTTGACAITIAA CAGTCATAGTGGGGAAAATAGGATTAITCCTTTAGCICGATAAGCAACCAGAAGTICTTCCTTCAAATCTTGACAITIAA CAGTCATAGTGGGGAAAATAGGATTAITCCTTTAGCICGATAAGCAACCAGAAGTICTTCCTTCAAATCTTGACAITTAA 1650 1650 1650 1650 1650 1650 1760 1710 1760 1710 1760 1770 1760 1760 1770 1780	CAGTCATAGTGGGGAAAATAGGATTAITCCITIAGCICGATAAGCAACCAGAAGTTCTTCCTTCAAATCTTGA CAGTCATAGTGGGGAAAATAGGATTAITCCTTTAGCICGATAAGCAACCAGAAGTTCTTCCTTCAAATCTTGA 1650 1660 1670 1680 1770 1700 1700 1700 1700 TIGATTTTTGGAAAACTGTTTCCTATGAAGCTATCTCTGCCTGAAGGATTTTTTTT	(1548) 1548	1560	1570	1580	1590	1600	1610	1620	163
CAGTCATAGTGGGGAAAATAGGATTATTCCTTTAGCTCGATAAGCAACCAGAAGTTCTTCCTTC	CAGICATAGIGGGAAAATAGGAITAITCCITIAGCICGATAAGCAACCAGAAGITCT CAGICATAGIGGGAAAATAGGAITAITCCITIAGCICGATAAGCAACCAGAAGITCT 1650	O 7(1548) AATATAT 13 (306)	TCAGTCATAGI	1 8-4	GATTATTCC.	TIAGCICGA	TAAGCAACC 	AGAAGITCII	CCTICARATCITG.	ACAITIAAIC
ATTGATITTTGGAAAACIGITTCCTATGAAGCTATCTCTGCCTGAAGGAITTTTTTTTTACAATCCAGACTATAGAAGGAAAATTTGAAATTTTTTTT	1700 TTCTTTTA TTCTTTTA TTCTTTTA TTCTTTTA CTTACACC CTTACACC CTTACACC CTTACACC CTTACACC	15 (558) 16 (686) AATATAT sus(1548) AATATAT	TCAGTCATAGT		GATTATTCC	1 86 ⊟	TAAGCAACC TAAGCAACC	AGAAGITCII AGAAGIICII		ACATTTAATC ACATTTAATC ACATTTAATC
	TTCTTTTA TTCTTTTA TTCTTTTA TTCTTTTA CTTACACC CTTACACC CTTACACC CTTACACC CTTACACC	(1639) 1639	1650	1660	1670	1680	1690	1700	1710	172
TITCCTATGAAGCTATOTCTGCCTGAAGGATTITTCTTTTACAATCCAGACTATAGAAGGAA TITCCTATGAAGCACTATCTCTGCCTGAAGGATTTTTCTTTTACAATCCAGACTATAGAAGGAA Section 1760 1770 1780 1790 1800 1810 GTCAGAGTTITACTGACCAATTCCCACCTCTGCCCTTACACGGAAGTTTATGCCTGTT	TICITITA TICITITA TICITITA CITACACC CTTACACC CTTACACC	O 7(1639) ATCAGAS 13 (306) 15 (558)	A:TCA:TTTTC		CCTATCAAG(TATCTGC	CTGAAGGAT	TTTTCTTT 	CAATCCAGACTAT	#C##CC##C#
1740 1750 1760 1760 1810 1780 1790 1800 1810 1810 1810 1810 1810 1810 18	1790 1800 1810 CTIACACCIAACGGAAGITIAIGCOI	16 (777) ATCAGRA sus(1639) ATCAGAA	ATTGATTTTTG ATTGATTTTTG	€-4 [-1	rcctatgaals rcctatgaage	ATCTCTS ATCTCTG	TGAAGGAT TGAAGGAT	TITCITITA TITCITITA	CAATCCAGACTAT. CAATCCAGACTAT.	AGAAGGAAAI AGAAGGAAAI Section 2
ISGACTITCACCTCCATISGTCAGAGITITACISACCAATTCCCACCICIGCCTTACACCIAACGGAAGITTAISCCIG	CTTACACCTAACGGAAGTTTATGCCTG	(1730) 1730	1740	1750	1760	1770	1780	1790		
	ISGACITICACCICCATISSICAGAGITITACISACCAATICCCACCICISCCTIACACCIAACSSAAGITIAISCCI	SEQ ID NO 7(1730) CACAACC SEQ ID NO 13 (306) SEQ ID NO 15 (558)	IGGACTITCAC	3.5	े तदी १-५	SIGACCAATT	E	GCCTTACACC	TABCGGAAGITIA	(1-4 (1-4 (1-4

1911	0 1 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	Section 22 2002		2093	.662TT.	CGGATTT	FGGATTT Section 24	2184	T
1900	TCCCTAAA TCCCTAAA	1990 TCAATTAAG		2080	TAXCAGAGO 	AGGTAACAGAGCT	TAACAGAGCI	2170	OIICAGIGA)
1890		1980 FIAGOATOTA	TAGCATGTAT	2070	7	CACAGITAGG	CACAGITAGG	2160	CAGCATAAAGGGATCTTCAGTGA
1880	5-4 E-4	Section 2 1950 1960 1970 1980 1990 2002 1970 1980 1990 1990 1900		2060	SEQ ID NO 7(2003) TOTTARCOTTOTOTOTOTOTARAGAGATATTAGGATTCAGAGATTOTOCCAGGATCACAGTARGAGGAGCTGGATTATTAGGTARGAGGTGGATTATTAGGTARGAGGTGGATTATTAGGTARGAGGTGGATTATTAGGTARGAGGTGGATTATTAGGTARGAGGTGGATTATTAGGTARGAGGTGGATTATTAGGTARGAGGTGGATTATTAGGTARGAGAGGTGAGATTATTAGGTARGAGAGGTGAGATTATTAGGTARGAGAGGTGAGATTATTAGGTARGAGAGGTGAGATTATTAGGTARGAGAGGTAGAGATTATTAGAGAGATTAGAGAGATTAGAGAGATTAGAGAGATTAGAGAGAGATTAGAGAGATTAGAGAGATTAGAGAGATTAGAGAGATTAGAGAGATTAGAGAGATTAAGAGAGATTAGAGAGATTAGAGAGATTAGAGAGATTAGAGAGAGATTAGAGAGAGATTAGAGAGAGAATTAGAGAGAGAGAGAGAATTAG	TCTCCCAGGATCACASTT	TCAGAGATATTAAGAGATTCTCCCAGGATCACAGTTAGGTAACAGAGCTGGATTT Section 24	2150	TTGTATAACAIGTCACGAATTCAGCATAAAGGGATCTTCAGTGAT
1870	TCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	1960 TTTGTTTAT		2050	TTAAGAGAT	AGATATTAAGAGAT	TTAAGAGAT	2140	ATAACAIGICACGAATT
1860	GTTATIATERAGCARCITITATITE	1950 IIAATAAIAI		2040	TTCAGAGATA 	TICAGAGAIA	ITCAGAGATA	2130	A A C C C C C C C C
1850	ATGGTTGTTA	1940 ICITARCATA	 	2030	ARTATTAGGR	AAIAIIAGGA	AATATTAGGAT	2120	ACGIATATAC
1840	CAGITACAA CAGITACAA CAGITACAA	1930 15GTAAAAIT		2020	T T G A A G A G A G	TIGAAAGAG	TIGAAAGAG	2110	ACAGCTCTA.
1830	SEQ ID NO 7(1821) TCTTCACATACCCCAACAGTTACAA. EQ ID NO 13 (306)	(1912) 1912 1920 1930 SEQ ID NO 7(1912) CTRATCACARAGGATTGGTARATT	JID NO 13 (306) JID NO 15 (558) JID NO 16(1050) CTAAICACAAAAGAITGGIAAAAII Consensus(1912) CTAAICACAAAAGAIIGGIAAAAII	2010	T. I.	CETTOICITI	Consensus(2003) TCTTAACGTTCTTTTTTGAAAGAG	2100	SEQ ID NO 7(2094) TAGTCCAGGTCTGTCTACAGGTCTAACGTAT IEQ ID NO 13 (306)
(1821) 1821	821) TCTTCA 306) 558) 959) TCTTCA 821) TCTTCA	(1912) (1942 (1912) (TAAICAC)	306) 558) 050) CTRATC 912) CTAATC	(2003) 2003	003) TOTTAR 306) 558)	141) TCTTAA	003) ICITAA	(2094) 2094	094) TAGICC 306) 558) 232) TAGICC
(18	SEQ ID NO 7(1821) TCTTCACATACCCCAACAGTTACAAA SEQ ID NO 13 (306)	(18 SEQ ID NO 7(18	SEQ ID NO 13 (306) SEQ ID NO 15 (558) SEQ ID NO 16(1050) CTAAICACAAAAGAITGGIAAAAI	(20	SEQ ID NO 7(2003) TCTTARCGTTC SEQ ID NO 13 (306) SEQ ID NO 15 (558)	SEQ ID NO 16(1141) TOTTAACGITOTOTITTTGAAGAGAAIAITAGGA	Consensus(20	(20	SEQ ID NO 7(2094) TAGICCAGGICTGICTACAGCTCTAACGIATATACACCCI SEQ ID NO 13 (306)

SEQ NO 13, 15 and 16 against SEQ NO 7 $\,$

SEQ ID NO 7(2185) CAGGGGICAGCAACCTITTCTAAAAAGGACCAAAIAGTAAIAITTCAGGCTITGTGGACCCTATGGICICIAICAIAACIGITCAAAICAC SEQ ID NO 13 (306)	TTTTCTAAAAAGGA						2275
(1323) CAGGGGTCAGCAACCT (2185) CAGGGGTCAGCAACCT (2276) 2276		CCAAATAGTAA 	:ATTTCAGGC 	FIFGTGGACC	CTATEGICIC	TATCATAACIGIT	3AAAICAC
(2276) 2276	ITTICIAAAAAGGA ITTICIAAAAAGGA	CCAAATAGTAAT CCAAATAGTAAT	IATITCAGGCIT IATITCAGGCIT	ITTGIGGACC	ISISGACCCTATGGICTC IGIGGACCCIAIGGICIC	GGACCAAATAGIAATATITCAGGCITIGIGGACCCTAIGGICTCIAICAIAACIGIICAAAICAC GGACCAAAIAGIAAIAIIICAGGCIIIGIGGACCCIAIGGICICIAICAIAACIGIICAAAICAC - Section 26	CAAATCAC CAAATCAC — Section 26
	90 2300	2310	2320	2330	2340	2350	2366
SEQ ID NO 7(2276) CATSTAGTGTAAAAGGAGCCATAASCAAAATATAAACTAACGAATGTGGGCTGTTTTATGGGATTTTTTT FO ID NO 13 (306)	BAGCCATABGCAAA	ATATAAACTAA	CGAAIGIGGC	TGTTTTTGC	GATTITITI	AACICIIIAIII	ACAAAAGC
SEQ ID NO 15 (558)	 GAGCCATAAGCAAA GAGCCATAAGCAAA			I I ≪ E			 3088860 4CAAAAGC Section 27
(2367) 2367 2380	2390	2400	2410	2420	2430	2440	2457
SEQ ID NO 7(2367) AGGTGCCACATCAGAACTCACTTATGGGCCATAGTTCTCT SEQ ID NO 13 (306)	ACTERCITATEGEC	CATAGRECICT	SACCCCTGAC	CTGAGAAAAT 	CTTATATITA	GACCCTGACCTGAGAAATCTTATTTATGGACAACATTTAT	TAGACTGTGA
SEQ ID NO 15 (558)SEQ ID NO 16 (1505) AGGIGGCAGITCAGAACICACIIATGGGCCAIAG Consensus(2367) AGGIGGCAGAICAGAACICACIIAIGGGCCAIAG	ACTCACTTATGGGCACTCCACTTATGGGC		SACCCTGAC SACCCTGAC	CTGACCCCTGACCTGAGAAATCTTATATT CTGACCCTGACCTGA	1-4 H	 TATSGACAACATTTAGACTGTGA TATGGACAACATTTAGACTGTGA	SACTGTGR SACTGTGR
							Section 28
(2458) 2458 2470	2480	2490	2500	2510	2520	2530	2548
SEQ ID NO 7(2458) CITGCCAAGIAAGAACAAGAAGCTCTGTCAACTGAAGGTCAAGGCTGGAGITCTGAAAGCAAAGAGCIS SEQ ID NO 13 (306)	CAAGAAGCTCTGTC	AACTGAAGGTC	1266CTGGA6	TICIGARAGC	AAAGAGCTG] 	TOIGGIGITAAIGA	AATGATAAGTGAA
SECTIONO 15 (558)		AACTGAAGGTC/	AAGGCTGGAG	TTCTGABAGG	AAAGAGCTG3	CTECTCTTAATGATAAGT	 :AAGTCAB

SEQ NO 13, 15 and 16 against SEQ NO 7 $\,$

SEQ ID NO 7 (2549) ATAGITAAAGITAGAAGATCCAGITAIAAGAAGAATAATGACCATAGACITCTGAACAAGAAIGITCTGGCTTAGG SEQ ID NO 15 (306)
SITATAAGAAGCACAAAGAATAATGACCATAGACTCCTGAACAAGAATGTCTGGACTTCTGGCTTAG SITATAAGAAGCACAAAGAATAATGACCATAGACTCCTGAACAAGAATGTCTGGACTTCTGGCTTAG Setion 3 2670 273 2861013 286114 286114 286114 286114 286114 286114 286114 286114 286114 286114 286114 286114 286114 286114 286114 286114 286114 286114 286114 38611
2670 2680 2890 2700 2710 2720 AGITACCTAATCTCTCCAGGCCTCCATTTTCTTATCATTAATGAGATAATAAAGTATITI
CARGITACCTAATCTCTCCAGGCCTCCATTITCTTAICATTAAATGAAGATAATAAAAGTATITICC SAGITACCTAATCTCTCCAGGCCTCCATTITCTTAICATTAAATGAAGATAATAAAAGTATITICC SAAGITACCTAATCTCTCCAGGCCTCCATTITCTTAICATTAAATGAAGATAATAAAAGTATTTTCC SAAGITACCTAATCTCTCCAGGCCTCCATTITCTTATCATTAAATGAAGATAATAAAAGTATTTTCC SAAGITACCTAATCTCTCCAGGCCTCCATTITCTTATCATTAAATGAAGATAATAAAAGTATTTTCC SAGION 3 SA
CAAGTTACCTAATCTCTCCAGGCCTCCATTTTCTTATCATTAAATGAAGATAATAAAGTATTTTCC Saction 3 Section 3 2770 2780 2790 2800 2817
2770 2780 2790 2800

EXHIBIT F

align SEQID#10 against SEQID#11.apr

	(1) 1	10	50	30	40	20	90	20	Section 1
SEQ ID NO 11		1) ATTTGAATTGGTGAACTTAGTAAAG	CTTAGTAAAGCA	GACGGCICIC	ACCAATAAGG	GCAGGCAICA	TCCAATCTGI	CGAAAGCITG	CAGACGCTCTCACCAATAAGGGCAGCATCATCCAATCTGTCGAAAGCTTGAATAAAAGG
SEQ ID NO 13		⋖	SITAGIAAAGCA	GACGGCICIC.	ACCAATAAGG	GCAGGCAICA	TCCAATCTGI	CGAAAGCIIG	CAGACGGCTCTCACCAATAAGGGCAGGCATCATCCAATCTGTCGAAAGCTTGAATAAAACAAAAAG
SEQ ID NO 18 SEQ ID NO 15 SEQ ID NO 17 Consensus									
	(92) 92	100	110	120	130	140	150	160	170 182
SEQ ID NO 11		(92) AGGAAGGGAAAATTTGCTTCTTTC	{ ⊢	CITGAICTAG	TATATCATCT	TCTCCTGCCC	TIGGAIGIGA	AGIGGGCCIIC	CITAAACCA
SEQ ID NO 13		– – A A	SCIICIIIICII	CITGAICTAG	 TATATCATCT	TCTCCTGCCC	TTGGATGTG	 AGTGGGCCTTC	 TICTIGATCTAGTATATCATCTTCTCCTGCCCTTGGATGTGAGTGGGCCTTCAGACTTAAACCAGG
SEQ ID NO 15									
SEQ ID NO 17	(92)			 	 	 		 	
	(183) 183	190		210	220	230	240	250	260 Seculon 3
SEQ ID NO 11	(183) AGIT.	SEQ ID NO 11 (183) AGITACACCITIGGCITCCCIGGIT	TCCCIGGIICI	CAGTICTTIG	GACTIGGACT	GAATTACACI	GCCAGGITIC	CCIGGIICICC	CTCAGIICITIGGACIIGGACIGAAIIACACIGCCAGGIIICCIGGIICICCAGCIIGCAGAIGGC
SEQ ID NO 13	(183) AGTT.	SECTION 10 (1)	TCCCTGGTTCT		GACTTGGACT		GCCAGGITIC	CTGGTTCTCC	rcciggirciccagcirgcagaiggc
SEC ID NO 16 SEC ID NO 15	(E)								
SEO ID NO 17	ΞE		 	 	 	 			
Consensus (183)	(183)								

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2 ID NO 11 (2/4) AGA	(274) 274 280	290	300	310	320	330	340 E 40	350	364
SEQ ID NO 13 (274) A GAZ SEQ ID NO 16 (1) SEQ ID NO 15 (1)	TCATGGGACTCATGGGACT	SEQ ID NO 11 (274) AGATCATGGGACTTCTTGGCCTCCAT SEQ ID NO 10 (1)	ATAATIGIGT ATAATIGIGT ATAATIGI	GAGTCAATTT	CCATTTAATT	TACATATCCA	GTTATGCATH	TAAITGIGIGAGICAAITICCAITITAITIACAIAICCAGITAIGCAITGCTIAACAAIGGAGACA 	3A GA CA
SEQ ID NO 17 (1) Consensus (274) (365) 365	370	086	390	400	410	420	430	440	Section 5
SEQ ID NO 10 (1)									Section 6
(456) 456		470	480	490	500	510	520	530	546
SEQ ID NO 11 (456) CATCTAGGCTACATGGTGTAGCTTG SEQ ID NO 10 (1)	CTAGGCTACA	TGGTGTAGCT1	GTAACCTCAT	GATAAGTATG	TATAACATCA	TGATAAGTAT	GTATGTATCT	TAACCTCATGATAAGTATGTATAACATCATGATAAGTATGTAT	ATGTAG
SEQ ID NO 16 (1) SEQ ID NO 15 (1)									
SEQ ID NO 17 (1) Consensus (456)		 		 	 		 		

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	(547) 547	560	570	580	590	009	910	620	Section 7 637
SEQ ID NO 11 (547) SEQ ID NO 10 (1) SEQ ID NO 13 (306) SEQ ID NO 16 (1) SEQ ID NO 16 (1) SEQ ID NO 15 (1) SEQ ID NO 17 (1)	SEQ ID NO 11 (547) AAAAGGTACAGTAAAAATATGGTATASEQ ID NO 10 (1)	GTAAAATAT 	GGTATAATCT	TATGGGATCAC	CATCATATATATATATATATATATATATATATATATATA	GCAATCCIT	IGIAGACIG	AATCTTATGGGATCACCATCATATATGCAATCCTTTGTAGACTGAAATGTCATTGTGTGTG	Option (CATG
	(638) 638	650	099	670	089	069	700	710	728
SEQ ID NO 15 (1) SEQ ID NO 17 (1) Consensus (638)	(1)(1) (238)								Section 9
	(729) 729	740	750	760	770	780	790	800	819
SEQ ID NO 11 (729) TTG. SEQ ID NO 10 (1) SEQ ID NO 13 (306)	SEQ ID NO 11 (729) TTGACTCTATTTCAAAATTTATGGT SEQ ID NO 10 (1)	TTCAAAATTT.	ATGGTTTTGG'	TGAAACATATG	TGGAGATGGG	GCATAGGTG	TGTGAACTG	TTTGGTGAAACATATGTGGAGATGGGGCATAGGTGTGTAACTGGGATAGTGTCCTGCTGATGAAT	ATGAAT
SEQ ID NO 15 SEQ ID NO 17	(1) (1)								
Consensus (729)	(729)								

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align SEQID#10 against SEQID#11.apr

Section 10	CTCCCACA	1001	TTTAAATA	Section 121092	36CTGCAC
006	GGCAAAAC(066	CAGGATTC	1080	AGATACTA(
068	\GCACTTTAT	086	A G G G A T T A G G G A T T A G G G A T T A G G G A T T A G G G A T T A G G G A T T A G G G A T T A G G G A T T A G G G G	1070	AAGTCTGGG
880	GCCCAGGGCATCAGCTTATAGATATCAAGAGCTCAACAAGAGCACTTTATGGCAAAACCTCCCACA	970	TTATGACAGATGACATTTATGGATAAAATAGGGATTAGCAGGATTCTTTAAATA	1050	ACCAGGCAGTGGGGCCCCCAAGTGCAGGGCCATAGGAAGTACAAGTCTGGGAGATACTAGGCTGCAC
870	ATATCAAGAG	096	ATGACATITA	1050	D D D D D D D D D D D D D D D D D D D
860	CAGCTTATAG	950	TTTATGACAG	1040	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
850	CCCAGGGCAT	940	CTAAAAGITICT	1030	CCAGGCAGT
840	TTGGGACAAG	930	SAGAAACTGC	1020	TTCATTTCTA
830	SEQ ID NO 11 (820) GGGTGGGAGGCATCATTTGGGACAA SEQ ID NO 10 (1)	920	SEQ ID NO 11 (911) AGACCTCTCAGAAGTTGAGAAACTG(SEQ ID NO 10 (1)	1010	SEQ ID NO 11(1002) CTTTCGAACACTAACCTTCATTTCT SEQ ID NO 10 (1)
(820) 820	(820) GGGTGG (1) (306) (1) (1) (820)	(911) 911	(911) AGACCT (1) (306) (1) (1) (1)	(1002) 1002	(1) (1) (1) (1) (1) (1)
	SEQ ID NO 11 (820) SEQ ID NO 10 (1) SEQ ID NO 13 (306) SEQ ID NO 16 (1) SEQ ID NO 15 (1) SEQ ID NO 17 (1) Consensus (820)		SEQ ID NO 11 (911) AGA SEQ ID NO 10 (1) SEQ ID NO 13 (306) SEQ ID NO 16 (1) SEQ ID NO 15 (1) SEQ ID NO 17 (1) Consensus (911)		SEQ ID NO 11(1002) CTTTC SEQ ID NO 10 (1) SEQ ID NO 13 (306) SEQ ID NO 15 (1) SEQ ID NO 15 (1) SEQ ID NO 17 (1) Consensus(1002)

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align SEQID#10 against SEQID#11.apr

- Section 13 - TACTAGT - 1183 - TACTAGT	1
T	
1170 TCTAAA 1260 TTAAAT TTAAAT	
ATAAT	
1160 1250 1250 1340 1340	
DO T T T G C C A T T T G C C A T T T T T T T T T T T T T T T T T	
1150 AATTATT 1240 IGTTGTG 1330 ATGAAAA	
1120	
114 CAGITIG 1230 LTCTAAA 1320 LTGAAIT	
1130 GAAAIG 	
11 122 122 123 124 1310	
1210 1210 1210 1210 1300 1300	
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	
1110 TGAAA/ 1200 CCTGAA/ CCTGA	
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	
1100 1190 1190 1190 1280 1280 1280 1280	
(1093) 1093	(1) (5)
(1093) 2) ID NO 11 (1093) 2) ID NO 10 (1) 3) ID NO 13 (306) 3) ID NO 17 (1) 3) ID NO 17 (1) 4) ID NO 10 (1) 5) ID NO 10 (1) 5) ID NO 10 (1) 6) ID NO 10 (1) 7) ID NO 10 (1) 8) ID NO 11 (1275) 9) ID NO 11 (1275) 9) ID NO 10 (1) 10 ID NO 11 (1275) 11 ID NO 11 (1275) 2) ID NO 10 (1) 3) ID NO 10 (1) 4) ID NO 10 (1) 5) ID NO 10 (1) 6) ID NO 10 (1) 7) ID NO 10 (1) 8) ID NO 10 (1) 9) ID NO 10 (1) 10 ID NO 10 (1) 11 ID NO 10 (1) 11 ID NO 10 (1) 12 ID NO 10 (1)	Q ID NO 17 (1) Consensus(1275)
SEC ID NO 11 (103) 1053 1100	SEQ ID NO 17 Consensus(

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align SEQID#10 against SEQID#11.apr

Section 16 1456	ACTTAGGGTATITCATGGCCCTAGTCTTTGGGGTACCACATGTTTCTTCTTCAAATCACAGATTCA	1547	CACTGAGAGITI	1638	TTTAAGTACATG
1440	TCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT	1530	TCTATGGAAC	1620	TAGACACAAT
1430	ACCACATGIT	1520	CTTCTGTCAT	1610	TTTTGGCTTTTT
1420	H	1510	AAATTGCTTG	1600	CTGGAATATT
1410	ATGGCCCTAG	1500	AAGTGAACCA.	1590	CAACTICAIG
1400	AGGGTATTTC	1490	TAGACAAAT.	1580	AACAGAGIGI
1390	STAAATACTT	1480	AGTGATTGTG	1570	GAATAGTAA
1380	AAGGACTCAGG	1470	ATGATAACACACACACACACACACACACACACACACACAC	1560	TTAAAATTT
(1366) 1366	SEQ ID NO 11(1366) CTGACTCTTAAGGACTCAGGTAAAT SEQ ID NO 10 (1)	(1457) 1457	SEQ ID NO 11(1457) AAATCAAGAATGATAACACAGTGATTGTGTAGACAAATAAGTGAAACCAAAATTGCTTGC	(1548) 1548	SEQ ID NO 11(1548) TTACTTGTGCTTAAAATTTTTGAATAGTAAAACAGAGTGTCAACTTCATGCTGGAATATTTTTGGCTTTTTAGACACAATTTTTAAGTACATG SEQ ID NO 10 (1)

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Section 19 1729 36AATCA	1820	SAT CCAC	1911	1.6GAAAAC
CTAAAGAGC	1810	IAACAAAIG	1900	AGCATGTAP
1710 GTTATAAAA(1800	GGAAGGAGT.	1890	CTGGGTCAGGGTCAGGGTCAGGGTCAGGGGGTCAGGGGTCAGGGGTCAGGGGTCAGGGGTCAGGGGTCAGGGGTCAGGGGTCAGGGGTCAGGGGGGTCAGGGGGTCAGGGGGTCAGGGGGTCAGGGGGTCAGGGGTCAGGGGTCAGGGGGTCAGGGGGGGTCAGGGGGGTCAGGGGGGGG
1700 ACTGGTATTT	1790	GAATAGAGGA 	1880	GCTCAGCTTGGCTTCAGCTTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG
1690 ICTTTTTAAA 	1780	TTACAGGATTATTACTGAAAAAGAAATGTACGGAATAGAGGAGAAGGAGTTAACAAATGATCCAC	1870	SACAGAGCT 1 1 1 1 1 1 1 1 1
1680 ACAGCITICI	1770	ACTGAAAAA	1860	AGTGCCTAA
1670 ACTGAAATTA	1760	CAGGATTATI	1850	GCTTTCCAGGA
1660 AAGTAACATC	1750	CTGATTAITA 	1840	CAATAAGCCT
1650 TTACAAGACT 	1740	ATAATTATTA 	1830	GTTGAAAACACACACACACACACACACACACACACACACA
(1639) 1639 (1639) AAGTATTT (1) (306) (1) (1) (1) (1)	(1730) 1730	0) AGAAAAGC 1)	(1821) 1821	(1) TCTGGGGTGGGTGGGGTGGGGTGGGGTGGGGTGGGGTG
Section 19 1639 1650 1660 1670 1680 1690 1710 1729 1	(173)	SEQ ID NO 11(1730) AGAAAAGCATAATTATTACTGATTA SEQ ID NO 10 (1)	(182	SEQ ID NO 11(1821) TCTGGGTGTTGAAAACACCAATAAGCCTGCTTCCAGGAAGTGCCTAAGACCAGAGCTGGCTCACGGGTCACAGGATGTAAGGAAAC SEQ ID NO 10 (1)

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align SEQID#10 against SEQID#11.apr

Section 22 2002	SCTGACA	2083	NCTATTA	2184	TCAGGC
1990	TTATGATATAG	2080	TATGTATACCA	2170	AGGCTATTAAC
1980	TAATCTTTAA	2070	ATAACCCAAP	2160	TAGTCACCCI
1970	CATGGGGAAA	2060	TTTTTCATAP	2150	TTAAGACTGC
1960	CC C A T A G C C C A T A G C C C A T A G C C C A T A G C C C A T A G C C C C A T A G C C C C C C C C C C C C C C C C C C	2050	GTCAAATTTA	2140	CTAACCCAAAG
1950	3ATAGATAAT	2040	ATTAACTTTT	2130	STTTAAATAT
1940	AGTIGICCA(2030	TTTATGTGAA	2120	GCTCCTAAAC
1930	CACCATCCATCCATCCATCCATCCATCCATCCATCCATC	2020	TGCTAAGICC	2110	GAGAAACTGA
1920	66CTACATG	2010	CAAAGCACTA	2100	CCTTAAAGAG
(1912) 1912	SEQ ID NO 11 (1912) TGCTGGGCTACATGCCACCATCCTCAGATAGATAATCCCATAGGGGAAATAATCTTTAATTATGATATAGCTGACA SEQ ID NO 10 (1)	(2003) 2003	SEQ ID NO 11(2003) CCATTCAAAGCACTATGCTAAGTCCTTTATGTGAATTTATTT	(2094) 2094	SEQ ID NO 11(2094) TCCTACCTTAAAGAGGAGAAACTGAGCTCCTAAAGTTTAAATATCTAACCCCAAGTTAAGACTGCTAGTCACCCTAGGCTATTAACTCAGGC SEQ ID NO 10 (1)
	S S S S S S S S S S S S S S S S S S S		S S S S S S S S S S S S S S S S S S S		S S S S S S S S S S S S S S S S S S S

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align SEQID#10 against SEQID#11.apr

(2185) 2185 2190	2200	2210	2220	2230	2240	2250	2260	2275 == 2275
SEQ ID NO 11(2185) AGTCTAACTCAGGTATAATAACATTA SEQ ID NO 10 (1)	AGGTATAATAA 	CATTATGCTA	CTGTTTGCAG	CTTTGACTAT	GCCTGAATT/	ATAACGTCAT(ATGCTACTGTTTGCAGCTTTGACTATGCCTGAATTATAACGTCATGCTATCTAACTAA	AAAGCTAA
SEQ ID NO 15 (1)								Section 26
(2276) 2276	2290	2300	2310	2320	2330	2340	2350	2366
SEQ ID NO 11(22/6) GGGAAATAAAATGAGCCCATAGGGCTCAATTTCATAAAGGAGAAAATACTGGGGAAAAGTGATAATGCAGAGTTTAAAATATTSEQ ID NO 10 (1)	ATGAGCCATAG	660TCAATTI	CATAAAAGGA(3AGAAAATAC	TGGGGAAAAC	TGATAATGO	AGAGTTTAAAATA 	W
SEQ ID NO 17 (1) Consensus(2276)								
(2367) 2367	2380	2390	2400	2410	2420	2430	2440	2457
SEQ ID NO 11(2367) AAAGTGCCAGAGATTGAGTATAACA. SEQ ID NO 10 (1)	AGATTGAGTAT	AACAAGTGTG	ACCAAAAAAA	AAAAAAAA 	AAAAAAGG! 	AAGAAGGTAA <i>i</i> GAAGGTAA <i>i</i>	AGTGTGACCAAAAAAAAAAAAAAAAAAAAAAGGAAGGAAG	STCTGAGA
SEQ ID NO 13 (306)								
SEQ ID NO 15 (1)								
SEQ ID NO 1/ (1) ========= Consensus(2367)	 	 			 	·		

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(24	(2458) 2458	2470	2480	2490	2500	2510	2520	2530	Section 282548
SEQ ID NO 11(2458) AATAGA. SEQ ID NO 10 (30) AATAGA. SEQ ID NO 13 (306) SEQ ID NO 16 (1) SEQ ID NO 15 (1) SEQ ID NO 17 (1) SEQ ID NO 17 (1)	SEQ ID NO 11(2458) AATAGAAATATCAGAGGAAGGAAAT. SEQ ID NO 10 (30) AATAGAAATATCAGAGGAAGGAAAT. SEQ ID NO 13 (306)	ATCAGAGGAA ATCAGAGGAA ATCAGAGGAA ATCAGAA ATCAGAA ATCAGAA	GGAAATAAA(GGAAATAAA(3GAGGGTGAGA 3GAGGGTGAGA 	GTAAATTCT(GTAAATTCT(CTTTTAGCATT CTTTTAGCATT	CAGATTCCAC, CAGATTCCAC,	SEQ ID NO 11(2458) AATAGAAATATCAGAGGAAATAAAAGGAGGGGGGGGAGAATTCTCTTTTAGCATTCCACAGATTCCACAAATCACATTTCT SEQ ID NO 10 (30) AATAGAAATATCAGAGGAAATAAAGGAGGGGGGGGGGGG	CATTICI
(25	(2549) 2549	2560	2570	2580	2590	2600	2610	2620	– Section 29– 2639
SEQ ID NO 11(2549) SEQ ID NO 11 (2549) SEQ ID NO 13 (306) SEQ ID NO 16 (1) SEQ ID NO 15 (1) SEQ ID NO 17 (1)	SEQ ID NO 11(2549) TITITIACCAACTAAGGAAAATAACACTTGACCTAACATTTCATTGCAGTTAGCTAAAGGATGCTAGAAAACTATGT SEQ ID NO 10 (121) TITITIACCAACTAAGGAAAATAACACTTGACCTAACATTTCATTGCAGTTAGCTAAAGGATGCTAGAAAACTATGT SEQ ID NO 13 (306)	AACTAAGGAA.	AAATAACAC:	ITGACCTAACA	TTTCATTGC/	AGTTAGCTAAA AGTTAGCTAAA 	GGATGCTAGA	SEQ ID NO 11(2549) ITITITACCAACTAAGGAAAATAACACTTGACCTAACATTTCATTGCAGTTAGCTAAAGGATGCTAGAAAAACTATGTTGCAGTTGGTTTG SEQ ID NO 13 (306)	TGCAGTGGTTTG
									- Section 30
(26	(2640) 2640	2650	2660	2670	2680	2690	2700	2710 2720	2730
SEQ ID NO 11 (2940) CTCT SEQ ID NO 10 (212) CTCT SEQ ID NO 13 (306) SEQ ID NO 16 (1)	940) CTCTAATTT 212) CTCTAATTT 306) (1)	CITCAGGAAL. CITCAGGAAL. 	AGAGAAAAG: AGAGAAAAG: 	GACAAAAGA GACAAAAAGA 	TCAGAGAAG! TCAGAGAAG! 	4GAAGAAAGGA 4GAAGAAAGGA 	AACTATCAGAA AACTATCAGAAA 	SECTIONO 11(2040) CTCTAATTTCTTCAGGAATAGAGAAAAGTGACAAAAGATCAGAGAAGAAAGGAAACTATCAGAAAAATACAGAATTGGAGTAGGA SECTIONO 10 (212) CTCTAATTTCTTCAGGAATAGAGAAAGTGACAAAAGATCAGAGAAGAAAGA	3AGTAGGA 3AGTAGGA
SEQ ID NO 15 SEQ ID NO 17	(1)								
Consensus(2640)	340)								

align SEQID#10 against SEQID#11.apr

(2731) 2731	2740	2750	2760	2770	2780	2790	2800	2810	Section 31 2821
SEQ ID NO 11(2731) TATAACATATITGGGTTGAAGGTAA. SEQ ID NO 10 (303) TATAACATATITGGGTTGAAGGTAA. SEQ ID NO 13 (306)	AACATATTTGGG AACATATTTGGG 	TTGAAGGTAA/ TTGAAGGTAA/ 	AAITITATATTGTAATCTTAAGTATCTTGCTACTTCAGTTTGGTCCCTGGAACAGCAGCATCAGAA AAITITATATTGTAATCTTAAGTATCTTGCTACTTCAGTTTGGTCCCTGGAACAGCAGCATCAGAA	GTAATCTTAA GTAATCTTAA 	GTATCTTGCT GTATCTTGCT 	TACTICAGIT: TACTICAGIT:	TGGTCCCTGGAACAGCAGCATCAGAA TGGTCCCTGGAACAGCAGCATCAGAA	AACAGCAGCA AACAGCAGCA 	TCAGAA
(2822) 2822	2830	2840	2850	2860	2870	2880	2890	2900	2912
SEQ ID NO 11(2822) TCTGCCGAGGGCTTGTTAAAAAGGCAGAATCTCCAGGTCCCATCCCAGACTCAGAATATAAATACTGACAAGATGCCCCGGGAT SEQ ID NO 10 (394) TCTGCCGAGGGCTTGTTAAAAAGGCAGAATCTCAGGTCCCATCCCAGACTCCAGAATATAAATACTGACAAGATGCCCCGGGAT SEQ ID NO 13 (306)	SCCGAGGGCTTG SCCGAGGGCTTG SCCGAGGGCTTG SCCGAGGGCTTG	TTAAAAAGGC/ TTAAAAAGGC/ 	AGAATCTCAGG AGAATCTCAGG	TCCCATCCCA TCCCATCCCA	GACTCACTGA GACTCACTGA 	ATCAGAATA'	FAATACTGAC	AAGATGCCC AAAGATGCCC AAAGATGCCC AAAAAAAAAA	CGGGAT
0.000		0000	0.00	C U	0000	00	0000		Section 33
SEQ ID NO 11(2913) Z913 Z920 SEQ ID NO 11(2913) TCATATGCACAGTAGAGCTGGCGAA	ZYZU IATGCACAGTAG IATGCACAGTAG	Z930 AGCTGGCGAA(AGCTGGCGAA(Z340 Z350 Z350 Z350 Z350 Z350 Z370 Z370 Z350 Z350 Z350 Z350 Z350 Z370 Z370 Z370 Z370 Z370 Z370 Z370 Z37	ZSDU GCCTGTGATT GCCTGTGATT	ZYBU GITITCIGCA GITITCIGCA	ZUVU ACTTAGTAT ACTTAGTAT	ZSBU FICTGAGITIT	ZYYU FCCCAAGGAA FCCCAAGGAA	3003 GAAAAC GAAAAC
SEQ ID NO 13 (306) 1 SEQ ID NO 16 (1) 1 SEO ID NO 15 (1) 1									
SEQ ID NO 17 (1)									
Consensus(2913)									

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align SEQID#10 against SEQID#11.apr

Section 34 3094	TGCCTGAG	3185	CCCTCCCTCCCTA	CATICCICIAITIA CATICCICIAITIA Section 36	3276	CTAACTCT CTAACTCT CTAACTCT CTAACTCT
3080	GIGITICICCITTACTTACTAGCTGCATGACTCATGAGCAAGGAAATCAAACTTTATGTGCCTGAGGTGTTTTCTCCTTTATGTGCCTGAGGTTTTTTTT	3170	TGAGGATGTTCAACAAATGCTCCTTTCATTCGTCTATTTA TGAGGATGTTCAACAAATGCTCCTTTCATTCCTCTATTTA	CCTIT	3260	AGCAGCCTTIGISCIALIAICIGIITICIAAACITAGIAALIGAGIGIGAICTGGAGACTAACICT AGCAGCCTTIGIGIALTATCIGIITICIAAACITAGIAAIIGAGIGIGAICTGGAGACTAACICI AGCAGCCTTIGIGIALTATCIGIITICIAAACITAGIAAIIGAGIGIGACTATCTGGAGACTAACICI AGCAGCCTTIGIGIATTATCTGTITTCIAAACITAGIAAIIGAGIGIGATCTGGAGACTAACICI
3070	AGCAAGGAAAT AGCAAGGAAAT	3160	ATAATAATCATCTCCTAGGCTTGTTTTGAGGATGTTCAACAAATGCTCCTTTCATT ATAATAATCATCTCCCTAGGCTTGTTTTGAGGATGTTCAACAAATGCTCCTTTCATT	TCAACAAAIGCI TCAACAAAIGCI	3250	GTAATIGAGIG GTAATIGAGIG
3060	CATGACTCATG	3150	TTGAGGATGTT TTGAGGATGTT	AIGIT	3240	TICIAAACITA TICIAAACITA
3050	TTACTAGCTG	3140	TAGGCTTGTT		3230	ATTATCTGTT ATTATCTGTT
3040	TCTCCTTTACT TCTCCTTTACT TCTCCTTTACT TCTCCTTTACT TCTCCTTTACT TCTCCTTTACT TCTCTTTACT TCTCTTTTACT TCTCTTTTACT TCTCTTTTACT TCTCTTTTACT TCTCTTTTACT TCTCTTTTTTTT	3130	ATAATAATCATCTCCTAGGCTTGT ATAATAATCATCTCCTAGGCTTGT		3220	AGCAGCCTTIGIGCTALTAICTGI AGCAGCCTTTGTGCIALTAICTGI
3030	NGACTIGIGIT NGACTIGIGIT	3120	3AGACTATAAT 3AGACTATAAT 		3210	CTGCTAGCAGCAGCTGCTAGCAGCAGCTCTTTTTTTTTT
3020	AGCTTCTGGCA	3110	CTATAAAATGG		3200	3186) CAGACCIGCCGCAGACAATICI (758) CAGACCIGCCGCAGACAATICI (306)
3004 3010	04) CCAGGCCTI7 76) CCAGGCCTI7 06)	(3095) 3095 3100	TTTCCTCATC		3186	86) CAGACCIGC 88) CAGACCIGC 16) (1) 86) CAGACCIGC 86) CAGACCIGC 86) CAGACCIGCC
(3004) 3004	SEQ ID NO 11(3004) CCAGGCCTTAGCTTCTGGCAGACTT SEQ ID NO 10 (576) CCAGGCCTTAGCTTCTGGCAGACTT SEQ ID NO 13 (306)	(3082)	SEQ ID NO 11(3095) TITCCTCATCTATAAAATGGAGACT SEQ ID NO 10 (667) TITCCTCATCTATAAAATGGAGACT SEQ ID NO 13 (306)	SEQ ID NO 17 (1) Consensus(3095)	(3186) 3186	SEQ ID NO 11(3186) CAGACCTGCCGCAGACAATTCTGCT SEQ ID NO 10 (758) CAGACCTGCGCGCAGACAATTCTGCT SEQ ID NO 13 (306)

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)GAAAT?)GAAATA	SEQ ID NO 11(3277) GAAATAAATAAGCTGATTATTTATT SEQ ID NO 10 (849) GAAATAAATAAGCTGATTATTTATT	3300 ATTTATTATT ATTTATT	3310 TTCTCAAAAC TTCTCAAAAC	3320 Jaacagaatac Jaacagaatac	3330 CGATTIAGCAA CGATITAGCAA	3340 ATTACTTOF.	0 3310 3320 3330 3340 3360 3350 3360 3350 3367 3367 3367 3367 3367 3367 3367 336	3367 CATTICIA CATITCIA
SEQ ID NO 13 (306) SEQ ID NO 16 (1) SEQ ID NO 15 (1) SEQ ID NO 17 (127) Consensus(3277)	06) (1) (1) 27) GAATA 77) GAAATA	SEQ ID NO 13 (306)		TTCTCAAAC	ARCRGARIAC		ATTACITCT		
(3368)	(3368) 3368	3380	3390	3400	3410	3420	3430	3440	3458
SEQ ID NO 15 (1) SEQ ID NO 17 (218) Consensus(3368)	(1) 118) TATICI 168) TATICI	SEQ ID NO 15 (1)SEQ ID NO 17 (218) TATICICCIACCIGAGITGAIGIG Consensus(3368) TATICICCIACCCIGAGIIGAIGIG	roalcicad rgaigigigag	CAATATGICA CAATATGICA	 .cttcataa? .cttcataa?	AGCCAGGTATA AGCCAGGTATA	 .CATTATGGAC .CATTATGGAC		
(3429)	(3459) 3459	3470	3480	3490	3500	3510	3520	3530	3549
SEQ ID NO 11(3459) TTR SEQ ID NO 10(1031) TTR SEQ ID NO 13 (306) SEQ ID NO 16 (1)	459) TTATIC 331) TTAIIC 306)	TACCT	CARABATITIA PARABITITA 	AATTTCAACT	6116060616	GTGTTGGTAAT GTGTTGGTAAT	GTAAAACAAA GTAAAACAAA 	TTTAAATTTCAACTGTTGCGGGGGGTGTTGGTAATGTAAAACAAAC	ATTCAGTA ATTCAGTA
•	(1) 309) TTATIC	CIACGITITIGICCAAAAI		TITAXATITCAACTGI					

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TATITAAGCCCCTGTACTTAAACATATTCCTCGTACCAATGAAGTTACATGAAAGCAAATTTGTGTGAGATATCGTAGATGAAGAATTTAAGCATTATCGTAGATGAATGA	(3550) 3550	3560	3570	3580	3590	3600	3610	3620	3630	3640
3670 3680 3700 3710 3720 TGAAATGCATTTCAAAAACTCTGTGTGTGTGTGTGTGTGT	Q ID NO 11(3550) CAGT Q ID NO 10(1122) CAGT Q ID NO 13 (306) Q ID NO 16 (1) Q ID NO 15 (1)	FATTTAAGCCCCT FATTTAAGCCCCT	GTACTTAAACA	TATTCCTCGT# TATTCCTCGT#	ACCAATGAAGT ACCAATGAAGT 	TACATGAAF TACATGAAF 	AGCAAATTTG AGCAAATTTG	TGTGAGATATC TGTGAGATATC 	GTAGATGGA/ GTAGATGGA/ 	4. 4. 1 1 1 D D 1 1 1
3670 3700 3710 3720 IGAAAIGCAITICAAAAACTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	Consensus (3550)								Sect	 ion 4
IGAAATGCATTTCAAAAACTCTGTGTGTGTGTGTGTGTGTG	(3641) 3641	3650	3660	3670	3680	3690	3700	3710	3720	3731
3760 3810 0000 3770 3780 3790 3800 3810 0000 3810 0000 0000 0000 000	© ID NO 11(3641) AATT © ID NO 10(1213) AATT © ID NO 13 (306) © ID NO 16 (1) © ID NO 15 (1) © ID NO 15 (1) © ID NO 17 (367) Consensus(3641)	FAGICITIAIGII FAGICITIAIGII	CCCCACAAATT(CCCCACAAATT(GAAATGCATTT GAAATGCATTT 	CAAAAACTC1 CAAAAACTC1 	161616161617 161616161617 1616161617 16161616	NTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG	TGACAGAGTGT TGACAGAGTGT	GTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	4 G G A B G G G A B G G G A B G G G A B G G G G
CCATAAGCTGGCTGTATGATTAATAAGACCAAGTTTTCTAAAGAAAATGAGATCATAACAAA	(3732) 3732	3740	3750	3760	3770	3780	3790			333
Q ID NO 16 (1)	Q ID NO 11(3732) ACAG Q ID NO 10(1304) ACAG O ID NO 13 (306)	SAGAGATACGCTT SAGAGATACGCTT	(7 (7)	ATAAGCTGGCT ATAAGCTGGCT	GCTATGATTA GCTATGATTA	AATAAGACCA AATAAGACCA	AGTTTTCTAA AGTTTTCTAA	AGAAAATGAGA AGAAAATGAGA	TCATAACAA) TCATAACAA) 	AAG AAG
Q ID NO 17 (367)	Q ID NO 16 (1)									
	O ID NO 17 (367)									-

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SEC ID NO 10395 COLUMN 1039	(3823) 3823 (3823) 3823	3830	3840	3850	3860	3870	3880	3890	3900	3913
4 3920 3930 3940 3950 3960 3970 3980 3990 SOCIOLICAGAGIANICALICANO SOCIOLICAGAGIANICALICANO SOCIOLICAGAGIANICALICANO SOCIOLICAGAGIANICALICANO SOCIOLICAGAGIANICALICANO SOCIOLICAGAGIANICALICANO SOCIOLICAGAGIANICALICANICALICANICANICANICANICANICANICANICANICANICAN	O 10(1395) CCI O 10(1395) CCI O 13 (306)	CTTTATGA	CIAICIIIIAIC CTATCTTTTATC	AGGGGCAAAA AGGGGCAAAA	AGGAAAGAGA AGGAAAGAGA 	CARARCAGO Carardago 	ATGAAATGATC TITIOTTC	AGACCAAGT	SATUAAAATIUA SATUAAAATIUA 	TTCACAA TTCACAA
Section 3950 3960 3970 3980 3990 Section 399	10 16 (1) 10 15 (1)				 AGGAAAGAGA		ATGAATGATG	AGACCAAGT		TICACAS
1990 3950 3960 3970 3980 3990	40 17 (367) ensus(3823)		 		AGGAAAGAGA	CAAAACAGC	ATGAATGATG	AGACCAAGT	SATGAAAATTCA	TTCACAA
	(3914) 3914		3930	3940	3950	3960	3970	3980	3990	4004
IGGGTAATTCAGCAGCCTGTTACTATGGCTCTCTGGAGTGATAGCTAATGTAAATGAAGCCT Section Socion A050 4040 4050 4060 4070 4080 ACTCAGCCAATAATGCAATCCATTCAAAGCATTCGGGAAAAATTCAAAAGAATAAA ACTCAGCCAATAATGCAACAGAAATCCATTCAAAGCATTCGGGAAAAATTCAAAAGAATAAA ACTCAGCCAATAATGCAACAGAAATCCATTCAAAGCATTCGGGAAAAATTCAAAAGAATAAA	O 10(1486) 1538 O 13 (306) O 16 (1) O 15 (67) 1538 O 17 (367)		AAGAGTAATIC 	10111666178		-6112C1ALA		G1681860	9AIGIAAAIGAA 	
100	onsus(3914) I GA	TIGCITIC	 AAGAGTAATTTC	I [→	TICAGCAGCC	TGTTACTAT(GGCTCTCTGGA	GTGATAGCT		GCCTCTA Section 45
ACTCAGCCAATAATGCAACAGAAATGCATTCAAAGCATTCGGGAAAAATTCAAAAGAATAAATA	(4005) 4005	4010	4020	4030	4040	4050	4060	4070	4080	4095
ACTCAGCCAATAATGCAACAGAAATCCATICAAAGCATTCGGGAAAAATTCAAAAAAAAAA	10 11(4005) 8.8.8 10 10(1577) 8.8.8 10 13 (306)	GTGGATTA	TCCTGACAAGAA TCCTGACAAGAA 	TATACTCAGO TATACTCAGO	CANTANTGCA CANTANTGCA	ACAGAAATO(ACAGAAATO(CATTCAAAGCA CATTCAAAGCA	TTCGGGAAA TTCGGGAAA	AATTCAAAAGAA AATTCAAAAGAA	TABATAT TABATAT
	(1) 10 15 (158) 요원 10 17 (367)	K E E B B B B B B B B B			CARTARIGCA	ACAGRARTC:		TTCGGGAAA		전 단 단

Section 46	SAT GARA		GATGAR	GATGAA Section 47	4277	H H H H H H H H H H	AATGTCT Section 48	4368	TTGCAG TTGCAG		((((E
	CAGCCAG		CAGCCAG	CAGCCAG		H H H H H H H H H H H H H H H H H H H	TIGGCAA		ACCITTO ACCITTO	UTION	
7170	AAAATATC AAAATATC		TAAAAATATCCAGCCAGGATGAA	AAAATATC	4260	SANTGATC SAN	 GAATGATC	4350	IIITAAAA IIITAAAA		
7160	CTICCCIGACTAACAAGCAGCAAGTAAAAATATCCAGGCAAGAATGAAAA		SAAGCACTIA	CAAGCACTTA	4250	3AAATICTIT 3AAATICTIT 3AAATICTIT		4340	AATTGATTAG AATTGATTAG	ATTGATTAG	
, , , , , , , , , , , , , , , , , , ,	TARCAAGCAGC		CTAACAAGCAGCACT	AACAAGCAG	4240	NATICIAAGCC		4330	GGGTGTCAA/ GGGTGTCAA/	GGGTGTCAAA	
74.7			CTTCCCTGAC	TICCCIGACI	4230	AGGGACTCAG AGGGACTCAG 1 1 1 1 1 1 1 1 1 1	AGGGACTCAG	4320	TTTCATGAA TTTCATGAA	TITCAIGAA3	! ! ! ! ! !
7130			ACCTACGATCCATITC	ACCTACGATCCATTTCTTCCCTGACTAACAAGCAGCAAGCA	4220	ATTTTGTTIGGTCCCAGGGACTCAGATTCTAAGCCAAATTCTTGAATGATCTTGGCAAATGTCT ATTTTGTTIGGTCCCAGGGACTCAGATTCTAAGCCAAATTCTTTGAATGATCTTGGCAAATGTCT		4310	TATCTTGGAAAAAAGTTTCATGAATGGGTGTCAAAATTGATTAGTTTTAAAAACCTTTCTTGCAG TATCTTGGAAAAAAGTTTCATGAATGGGTGTCAAAATTGATTAGTTTTAAAAACCTTTCTTGCAG	TAICTIGGAAAAAAGTIICAIGAAIGGGIGICAAAAITGAITAGITITAAAAACCITIC	
00.17	AATCACCTAC		AATGACCTAC	AATGACCIAC	4210	TAATATITIT TAATATITIT TAATATITIT TAATATITIT	TAATATTTT	4300	TCTTTATCTT TCTTTATCTT	TCITIAICII	
7	SEQ ID NO 11(4096) TCTTTTTTTTAAAGTTAATS		ITTTTAAAGTTAATG	Consensus(4096) ICITITITITITIAAAGITAAIG	4200	SEQ ID NO 11(4187) ATAGAAACCCACCTGACTTGTTAAT SEQ ID NO 10(1759) ATAGAAACCCACCTGACTTGTTAAT SEQ ID NO 13 (306)	ID NO 17 (367)	4290	SEQ ID NO 11(4278) CGAATTATTTTTGCCAAGTTTTCTT SEQ ID NO 10(1850) CGAATTATTTTTGCCAACTTTTGTT SEQ ID NO 13 (306)	SEQIDING 18 (1)	
800			Signer	CITITITI	187	TAGAAACCCA		278	SGAATTATTTT SGAATTATTTT 		
4006 4006	T (4096) T (4096) T (101668)	SEQ ID NO 13 (306)	SEQ ID NO 15 (249) ICTITITE (250)	ensus(4096) T	(4187) 4187	SEQ ID NO 11(4187) ATAGAAAC SEQ ID NO 10(1759) ATAGAAAC SEQ ID NO 13 (306) SEQ ID NO 16 (1) SEQ ID NO 16 (300) ATAGAAAC	SEQ ID NO 17 (367)	(4278) 4278	SEQ ID NO 11(4278) CGAA SEQ ID NO 10(1850) CGAA SEQ ID NO 13 (306)	SEQ ID NO 18 (1) SEQ ID NO 15 (431) CGAA SEO ID NO 17 (367)	(350) / I OI DI DI
	SEQ ID P	SEQ ID P	SEQ ID P	Conse		SEQ ID P SEQ ID P SEQ ID P SEQ ID P SEQ ID P	SEQ ID P Consi		SEQ ID NO 11(4) SEQ ID NO 10(1) SEQ ID NO 13 (2)	SEQ ID	י שור אינו היינו

(4369) 4369	4369	4380	4390	4400	4410	4420	4430	4440		4459
SEQ ID NO 11(4369) ATRACGTATGGCACCCTAAAACTGTATTAGAAAAAG SEQ ID NO 10(1941) ATACGTATGGCACCCTAAAACTGTATTAGAAAAAAA SEQ ID NO 13 (306)	ATACGTS ATACGTA 	ATGGCACCTA ATGGCACCTA	AAACTGTATT AAACTGTATT	TTAGAAAAAAGTAGTACTCTGTAGTGTGAAAATTCTTAAAGACACCCTCTTTTACAAACTCA TTAGAAAAAAA	TAAGTACTCT	GTAGTGTGA/ 	AAATTCTTA? 	AAGGACACCCI 	CCTTTTACA	AACTC
SEQ ID NO 16 (1)SEQ ID NO 15 (522) ATACGTATEGCACCCTAAAACTGTA	(1) (522) atacgta	ATGGCACCTA	3	TAGAAAAAA-						
SECTIONOT/ (36/)	ATACGTA	 ATGGCACCCTAA	AAACTGTATT	 AGAAAAAA		 				Section 50
(4460) 4460	4460	4470	4480	4490	4500	4510	4520	4530	4540	4550
Consensus(4460)										Section 51
(4551)	4551	4560	4570	4580	4590	4600	4610	4620	4630	4
SEQ ID NO 10(1951) TGGCAGGTGTGGTGGTCACACCTGTAATTCCAGCACTTTGGGAGGCCAAGGCGGGGGGGATCACCTGAGATCAGGAGTTCAGGACCAGCCT SEQ ID NO 10(1977)	TGGCAGG	GIGIGGIGGCI	CTCACACCIGIA	ATTCCAGCAC	TTTGGGAGGC	CAAGGCGGG	GGATCACCTC	SAGATCAGGA(STICAGGAC	CAGC
SEQ ID NO 13 (306) SEQ ID NO 16 (1)	 									
SECTIONO 15 (558) - SECTIONO 17 (367) -	 									
Consensus(4551)										

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Section 52 4720 4732	TACTGAAAATACAAAAATCACCCGGGTGTGGGGGCGCCTGTAGTCCCAGCTACTCGGGTAGC	10 4823	GACAGAGCAAGA	4914	VGTCAATIGITITI
4710 4	TAGICCCAGC	0 4810	C A G C C T G G G T I I I I I I I I I I I I I I I	4900	TATTCACCCA
	GGGCGCCTG	4800	ACTGCACTC	4890	GCATGGAAA
0 4700	5TGTGGTGAC	4790	AGATCATGCC	4880	CO C C C C C C C C C C C C C C C C C C
4690	ATCACCCGGC	4780	AGTGAGCTG2	4870	CAGCTATTCC
4680	AATACAAAA.	4770	AGAGGITGC.	4860	GTTTTCAA
4670	TTTACTGAA	4760	TCAGGAGTC	4850	AAAAGACTG
4660	AAACCCAGTC	4750	TCACTIGAAC	4840	AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
4650	AATATGGTG,	4740	GCAGGAGAA	4830	ATCTCAAAAA
(4642) 4642	SEQ ID NO 11(4642) GATCAATATGGTGAAACCCCAGTCTT SEQ ID NO 10(1977)	(4733) 4733	SEQ ID NO 11(4733) TGAGGCAGGAGAATCACTTGAACTCAGGAGTTGCAGTGAGATCATGCCACTGCACTCCAGCCTGGGTGACAAGA SEQ ID NO 10(1977)	(4824) 4824	SEQ ID NO 11(4824) CTCCATCTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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align SEQID#10 against SEQID#11.apr

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(5188) 5188 5200 5210	5200	5210	5220	5230	5240	5250	5260	Section 58 5278
SEQ ID NO 11(5188) TCATGAA. SEQ ID NO 10(1977) SEQ ID NO 13 (306) SEQ ID NO 16 (1) SEQ ID NO 16 (558) SEQ ID NO 17 (367) Consens 15 (588)	ACCAGGTAP	AGAAAGIGGA	CTAGATTAATT	TCATCCATC	ACAGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA	GAGCCGTGAA	AGATAATCCAG	GGACTAGATTACATCCATTACAGGAAGAGCAGCCGTGAAAGATAATCCAGAAATCATTGGGA
(5279) 5279	5290	5300	5310	5320	5330	5340	5350	Section 59 5369
SEQ ID NO 10(1977)								
(5370) 5370	5380	5390	5400	5410	5420	5430	5440	5450 Section 60
SEQ ID NO 11(5370) TACCCATGAGTTGACTCAGAAAAACATAAAAAGTATTGTTGCTCTGCTCTGCTCTAACTCATTCTCACTTCTCATTTCCATGATG SEQ ID NO 10(1977)	GAGTTGACTCA	GAAAAAACAT.	AAAAAGTATTG	0	TCAGAGITIT	ATCTAACTCA	TTCTCACTTCT	TATTCCATGATG
SEQ ID NO 17 (367) Consensus(5370)								

align SEQID#10 against SEQID#11.apr

(5461) 5461	5470	5480	5490	5500	5510	5520	5530	5540	5551 5551
SEQ ID NO 11(5461) AAATGACATAAATGAGTTTTTTAT SEQ ID NO 10(1977)	3A CA TAAA TGA	16GTTTTTAT	TGTTGTTGTTGTT	TGTTGTTGTTGTTTTTTTTTTTTTTTTTTTTTTTTTTT	GGACACAAGC	CAAGGTAGC	TACCTGGGCA	GAGCTGTTTT	ATTICIC
(5552) 5552	5560	5570	5580	5590	5600	5610	5620	5630	5642
SEQ ID NO 10(1977)									
(5643) 5643	5650	5660	5670	5680	5690	5700	5710	5720	Section 635733
SEQ ID NO 11(5643) GCATCCTTCCCTGTCCTCAATTCCA SEQ ID NO 10(1977)		CCTCAATTCC	ATTGTTGGTG	TIGITGGTGATGACAATGTCTCTCCCATCAGCCTCATGAAGTTCTCTCTC	CTCTCCCATC	AGCCTCATG,	AAGITCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTC	TCATTTATTA TCATTTATTA	AAATTTG
Consensus (5643)									

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(5734) 5734 5740	5740	5750	5760	5770	5780	5790	5800	5810	Section 64 5824
SEQ ID NO 11(5734) CTTTCAGGAAAATTTTGAAAATGTG SEQ ID NO 10(1977)	CAGGAAAAA 	TTTGAAAAT(STGTCCAGTA	ATGCCTGATT	8GCCCCTTA 1	CCTAAAGGCT	AAACTGGAG	GTCCAGTAATGCCTGATTGGCCCCTTATCCTAAAGGCTTAAACTGGAGGAAGGA	AACTGAG
(5825) 5825 5830	5830	5840	5850	5860	5870	5880	5890	5900	5915
SEQ ID NO 11(5825) AAATCTTGCAAATCATTGAGCCAAA. SEQ ID NO 10(1977)	CTTGCAAAT	CATTGAGCCAA	AACGTAT	TAATAGCAAGATCTATCAT	TCTATCATTT	TTATTGACTAGTATGTGGCAGGCAGTGCCCT	ATGTGGCAGG	\vdash \vdash \vdash \vdash \vdash \vdash	TTATTTAG
Consensus(5825)									Section 66
(5916) 5916		5930	5940	5950	2960	5970	5980	5990	9009
SEQ ID NO 11(5916) GCAGGGAGAGTTGATGGGGGGGGGGGGGTTCACATCTTAAAGAGGTGCTATCTCCTCTATATAAATCATGTAAGTCAAGAGTAAGG SEQ ID NO 10(1977)	3GAGAGTTGA 	ATGGGGGGGG()	CGGGGTTCAC	ACATCTTAAA 	GAGGTGCTAT(CTCCTCCTATA	ATAAATCATG 	TAAGTCAAGAG 	AGTAAGG
SEQ ID NO 16 (1)									
SEQ ID NO 17 (367)									
Consensus(5916)									

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2009 (2009)	6020	0030	6040	6050	0909	6070	6080	- Section 67 6097
SEQ ID NO 11(6007) AATTGTCTTTGTTTGGTTATATTCA SEQ ID NO 10(1977)	TCTTTGTTTGGTT7	VTATICAGGGG	ATTAGAGTATATAGAGTATATAGAGTATATAGAGTATATAGAGTATATAGAGTATATAG	ACAGTAGAAG	ATCCCAAGAA	ACCTTGGGAT	GGGGATTAGAGTATACAGTAGAAGATCCCCAAGAAACCTTGGGATCATTTTAGACTAAGAAATGCCAAGAAATGCCAAGAAATGCCAAGAAATGCCAAGAAGAAAAGAAAAAAAA	AAATGCCA
8608 (8608)	6110	6120	6130	6140	6150	9160	6170	6188
SEQ ID NO 11(6098) ATACCGCCGGGCGCGCGTGCTCACGCCTGTAATCCCCAGCACTTTGAGAGGCCGAGGTGGGCGGATCACAAGGTCAGGAGATTGAGACCGTC	ecceeececeerec	SCICACGCCIG	TAATCCCAGC	ACTITGAGAG	GCCGAGGTGG	GCGGATCACA	AGGTCAGGAGATIG?	AGACCGIC
SEQ ID NO 10(1977) SEQ ID NO 13 (306)								
SEQ ID NO 16 (1)								
SEQ ID NO 17 (367)								
Consensus(6098)								Cootion 60
(6189) 6189	6200	6210	6220	6230	6240	6250	6260	6279 - 5401011 03
SEQ ID NO 11(6189) CTGGCTAACGTGGTGAAACCCTGTCTCTACTAAAATACAAAAATTAGCCGGGCGTGGTGGCGGGCG	TAACGIGGIGAAAC	CCTGTCTCTA	CTAAAAATAC	AAAAAATTAG	CCGGGCGTGG	TGGCGGCGC	CIGIAGICCCAGCI	ACTCGGGA
SEQ ID NO 13 (306)								
SEQ ID NO 16 (1)								
SEQ ID NO 15 (558)			 	 	 	 		
SECTION 17 (307) Consensus(6189)	 	 	 	 	 	 	 	

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(6280) 6280	6280	6290	6300	6310	6320	6330	6340	6350	6360	Section 70 6370
SEQ ID NO 11(6280) GGCGGAGGCAGGAATGGTGTGAA SEQ ID NO 10(1977)	2280) GGCGGAG 1977) (306) (1) (558)	3GCAGGAGAA1	GGTGTGAACT	CAGGAGGCGG	SAGCTTGCAG:	CTCAGGAGGCGGAGCTTGCAGTCAGCCGAGATTGCCCCAATGCACTCCAGCCTGGGCGACAGAACG	TGCCCCAATG	CACTCCAGCC	TGGGCGAC	AGAACG
Consensus (6280)										Section 71
(6371) 6371	6371	6380	6390	6400	6410	6420	6430	6440	6450	6461
SEQ ID NO 11(6371) AGACTCCGTCTCAGAACAAACAAA. SEQ ID NO 10(1977)	AGACTCC	CGTCTCAGAAC	CAAAACAAAAG.	GAAATGCCAA	ATACCAGCAG:	AGGAAATGCCAATACCAGAAATAGAGCCAAATCATGAACATAAGCTAAACAAATGTTGGCAGT	AATCATGAAC	ATAAGCTAAA	CAAATGTT	GGCAGT
(6462) 6462	5462	6470	6480	6490	6500	6510	6520	6530	6540	36011011 72 8552
SEQ ID NO 11(6462) GTAGCCTAGTGATAAGAGCAGACTCTTAACTAGAACACTGCACTCCATGTCCTCACTGTAGACCCTCACTGTGGGGTTCTAATTAACC SEQ ID NO 10(1977)	3462) GTAGCCT 1977) (306)	AGTGGTTAAGA	3AGAGCAGACT(CITAACTAGA	AACACTGCAC:	CCATGTCCTC	ACTGTAGACC	CTCACTGTGG	GGTTCTAA	TTAACC
SEQ ID NO 15 (558) SEQ ID NO 17 (367) Consensus(6462)										

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(6553)	39	6560 6570	6580	6590	0099	6610	6620	6630	Section 736643
SEQ ID NO 11(6553) CCTGTTACTTACCAGTGGCAGTCTT SEQ ID NO 10(1977)	T	TTACCAGTGGCAGT	4	CCTTAAGTTC	GTTGTGCCCC	AATTIGITCA	TCTGTAGAA(AGGCATTCCTTAAGTTCGTTGTGCCCCCAATTTGTTCATCTGTAGAAGGGGTAGGATGACAGTAGT	CAGTAGT
(6644) 6644	4 6650	0999	0299	6680	6690	6700	6710	6720	Section 746734
SEQ ID NO 11(6644) GITTACTITATAGGCTTACTGTGAGG	TIACIT	TATAGGCTTACTGT	GAGCATTAAATO	SAGITACIAC	CATTAAATGAGTTACTACTGTATTTGTAAAGTGCTTAAAATGCTGCTCCAAAAGAGT	AAGIGCITAA	AAIGCIGCIO	[⊢	TGTTAAAC
SEQ ID NO 10(1977) SEQ ID NO 13 (306)									
SEQ ID NO 15 (558)	 								
SEQ ID NO 17 (367) Consensus(6644)	 								
(6735)	5 6740	6750	6760	6770	6780	6790	6800	6810	Section 75 6825
SEQ ID NO 11(6735) ACTTAAGAACTGATTTACTTGCATC	TTAAGA	ACTGATTTACTTGC	ATCTAAACTGA	CAGCTCTCAA	TAACTGGAAA	IGATCAAGCA	TAGGCCCTGC	TAAACTGACAGCTCTCAATAACTGGAAATGATCAAGCATAGGCCCTGGAATATAAGCAGGTCTACA	GTCTACA
SEQ ID NO 13 (306) SEO ID NO 16 (1)									
SEQ ID NO 15 (558)									
SEQ ID NO 17 (367) Consensus(6735)	 								

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align SEQID#10 against SEQID#11.apr

(6826) 6826	6840	6850	0989	6870	6880	06890	0069	Section 76 6916
SEQ ID NO 11(6826) TGAAGGCAAAATGTTCGTTTCTTT SEQ ID NO 10(1977)	GGCAAAATGTTCG7	TTCTTTTGTTTTGTTTTTTTTTTTTTTTTTTTTTTTTT	CAGCCTGTG	CCTAGATCAA	FATCTAGTGA1	CATGCTCAA(TGTTCAGCCCTGTGCCTAGATCAATATCTAGTGATCATGCTCAAGAAATATTGTTGAATGAA	ATGAATCAA
(6917) 6917	0869	6940	6950	0969	6970	0869	0669	7007
SEQ ID NO 11(9917) 1GAACCTACCGAGGTAGTTACATAAAAGAGTSEQ ID NO 10(1977)	CCTACCGAGGIAGII	ACAIAAAGA	MOTICI GCA1G	4 G I A CAAA I I	1.666CAAAG I.C	2 P C C P P C C P P C C P P C C P P C C P P C C P P C C P P	ICIGCAIGAGIACAAAICIGGGCAAAGIGACCICCAAGGAAAIIICCACII	11AGA11C1
8002 (2008)	7020	7030	7040	7050	7060	7070	7080	7098 ––– Section 78
SEQ ID NO 11(7008) GIGATITICCITAAGGAACIGATAAA SEQ ID NO 10(1977)	TTTCCTTAAGGAAC1	$\exists \vdash \vdash \vdash \vdash$	TGGTGTGATACAATGTAAAAAATGTGCCTATATGATTTGAGAAAAACTTAT	IGTAAAAAAAT	GTGCCTATAT	GATTIGAGA/ 		CICICCCICI
SEQ ID NO 16 (1) SEQ ID NO 15 (558)								
SEQ ID NO 17 (367) Consensus(7008)								

align SEQID#10 against SEQID#11.apr

Section 79 7189	TCTTTTT	7280	GCCTTT	Section 81 7371	H
		7270	TTCTTTGT	7360	TCTTTCTTTCCTTCTTTTTTTTTTTTTTTTTTTTTTTT
7170	TTCCTTCTC	7260	CTTTCTTCCT	7350	1. GTTTTTCTT
7160		7250	CTTTCCTTT	7340	H
7150	CCTTCCTTCCTTCTTCTTCTTCTTCTTCTTTTTTTTTT	7240	CTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT	7330	CCTTTCTTTCTTTCTTTCTTTCTGCCTTTCTTTCTTTGTTTTT
7140	C	7230	TTCTTTCTTT	7320	
7130	TCCTTCCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT	7220	CTTTCTTTCT 	7310	
7120	CT C	7210	TTCTTTCTTT	7300	HOH
7110	TCCTTCCTTCTTCTTCTTCTTTCTTTCTTTCTTTCTTT	7200	CITTCTTTCT 	7290	C1111111111111111111111111111111111111
6602 (6602)	SEQ ID NO 11(7099) ITTITICCTTCCTTCCTCCCCCCCSEQ ID NO 10(1978)	(7190) 7190	SEQ ID NO 11(7190) CITTCITICITICITICITICITICITICITICITICIT	(7281) 7281	SEQ ID NO 11(7281) CTTTCTTTCTTTCTTTCTTCTCTCTCTGTS SEQ ID NO 10(1978)
	SEQ ID N. SEQ ID		SEQ ID NO SEQ ID	0.	SEQID NE SEQ

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TTTAAGCAGACCATGTCTGTT	7400 7410 7420 7430 7440 7450 7462 AGATGAATGCCTTTTTCTAGTTAAAAGGTTAAACAGGAAAGTGAAGCACAATTATCAAGGGTCTCC	7490 7510 7520 7530 7540 7553 TIAICITITIACAGITTCATATCTCCAGGCCTTTCATTGGGTCAGGTTGGCATTTCGCTGCCCT TTCATATCTCCAGGCCTTTCATTGGGTCAGGTTGGCATTTCGCTGCCCT	 TICATATCICCAGGCCTITCATIGGGTCAGGTIGGCATTICGCTGCCCT Section 84	7580 7600 7610 7620 7630 7644 66AAAGAAAAACTCAAGTGAAAATCAGAATCTGCGCAGCAGTTCCTGGGCGTTTCAGCTGC 66AAAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	GGAAAGAAAAAACICAAGTGAAGAAAATCAGAATUTGCGCAGCAGTTCGGGGCGTTTCAGGTGC
2 7380 CCTTTAAGCAGA CCTTTAAGCAGA CCATCTCCACAT CCATCTCCACAT CATGTGTGACA ATGTGTGTGACA ATGTGTGTGACA	7390 .CCATGTCTGTT 	7480 GIICITAAICA		7570 AGTGAAAATAA AGTGAAAATAA	AGTGAAAAIAA
SEQ ID NO 11(7372) 7372 SEQ ID NO 10(1978) SEQ ID NO 13 (306) SEQ ID NO 15 (558) SEQ ID NO 17 (367) Consensus(7372) SEQ ID NO 11(7463) 7463 SEQ ID NO 11(7463) AG1 SEQ ID NO 16 (1) SEQ ID NO 16 (558) Consensus(7463) Consensus(7463) SEQ ID NO 17 (367) Consensus(7463) SEQ ID NO 11(7554) 77554	SEQ ID NO 11(7372) 7372 7380 SEQ ID NO 11(7372) TTCCTTTAAGCAGA SEQ ID NO 10(1978) SEQ ID NO 13 (306) SEQ ID NO 15 (558) SEQ ID NO 15 (558) SEQ ID NO 17 (367) Consensus(7372)	(7463) 7463 7470 (7463) AGICAICICCACAI (1978)		(7554) 7554 7560 (7554) TTAIGIGIGACA (2027) TTAIGIGIGACA (306)	AIGIGIGIGACA

Section 85

8008	CATTTCAGCT	CATITCAGCI 	Section 89 8099	AGCTGCTTCT	# # # # # # # # # # # # # # # # # # #	AGCTGCTTCT Section 90	8180 8190	CICAAAGAAA CICAAAGAAA	TCTCAAAGAAA	
7990	SEQ ID NO 11(7918) TECCAAACACAGTECECTEATICICCCAAGAACCAGAATGTGACTGCTCACCICICTAAGGACCTGAAAACAACTGGCCATTICAGCT SEQ ID NO 10(2391) TECCAAAACACAGATCTCTCTTCCCAAGAAACCAGAATGTGACTGGTCACCTCTCTAAGGACCTGAAAACAACTGGCCATTTCAGCT SEQ ID NO 13 (306)	CCCAAGAACCAGAAIGTGACIGCICACCICICIAAGGACCIGAAAACAACIGGCCAITICAGCI 	8080	SEQ ID NO 11(8009) ATTTAAATCAACTITAAAAATCCAACGGCAAAATATTAAACCATTTTGGTTGGAATGATAACATAACTAAC	GGAAIGATAACTAACTGCTGCTGACAGCTGCTT		8170 81	SEQ ID NO 11(8100) GCTAGGTGCAAAAATGGAAAAAAAAAAAATACTTCTAATCAGGTCAAATCACTCTACCTTTGGGATTCTAAATTTACTCATATTCTCAAAGAAA SEQ ID NO 10(2573) GCTAGGTGCAAAAAAAAAAAAAAAAAAAATACTTCTAATCAGGTCAAATCACTCTACCTTTGGGATTCTAAATTTACTCATATTCTCAAAGAAA	TACTICTAATCAGGTCAAATCACTTTGGGGATTCTAAATTTACTCATATT	
7980	CTAAGGACCTE CTAAGGACCTE 	CTAAGGACCTC 	8070	GATAACATAAC GATAACATAAC		GATAACATAAC	8160	GGGATTCTAAA GGGATTCTAAA		
7970	redroaderer redroaderer	TGOTOACCTCT 	8060	TIGGITEGAAT FIGGITEGAAT	TGGTTGGAAT	 [TGGTTGGAAT	8150	ACTCTACCTTT ACTCTACCTTT		1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
7960	KGAATGTGACI AGAATGTGACI	X6AATGTGACT 	8050	TABACCATT	TAAACCATTITGGTT	TAAACCATT	8140	NGGTCAAATCA	AGGTCABATCZ	
7950	CCAAGAAACCA CAAGAAACCA	CAAGAAAC.A 	8040	GCCAAAATAT		 :GCCAAAATA1	8130	CTTCTAATO?	CTTCTAATCA	
7940	TTAATTCTCC TTAATTCTCC	TTAATTCTCT 	8030	ABATCCAACC	. A A A T C C A A C C	△;	8120	AAAAAAATE AAAAAAATE	KL	
7930	CACAGITCTC CACAGITCTC 	ACACAGTICIC 	8020	CAACITIAAA	CAACITIAAA		8110	CAAAAATGGA	CCAAAAATGGA	
(7918) 7918	(7918)	CCAAA 	6008 (6008)	SEQ ID NO 11(8009) ATTTAAATCAACTTTAAAAAATCCAA SEQ ID NO 10(2482) ATTTAAATCAACTTTAAAAAATCCAA	SEQ ID NO 15 (506) ATTTABATCABCITTABABATCCAB SEQ ID NO 15 (558)	ID NO 17 (367)	(8100) 8100	1(8100) GCTAGGTG 1(2573) GCTAGGTG	TACGT 	7 (367)
	SEQ ID NO 11(7918) IT SEQ ID NO 10(2391) IT SEQ ID NO 13 (306) –	SEQ ID NO 16 (415) TE SEQ ID NO 15 (558) SEQ ID NO 17 (367) Consensus(7918) TT		SEQ ID NO 10 SEQ ID NO 10	SEQ ID NO 15 (506) 5.T. SEQ ID NO 16 (506) 5.T. SEQ ID NO 15 (558)	SEQ ID NO 17 (367) – Consensus(8009) A		SEQ ID NO 10 SEQ ID NO 10	SEQ ID NO 13 (306) SEQ ID NO 16 (597) SS SEQ ID NO 15 (558)	SEQ ID NO 17 (367)

Section 91 8281	ABTCABT ABTCABT 	TWESTER	AATCAAT Section 92	8372	AAATTOR	AARITCA 	AAATTCA Section 93	8463		CTTCTC	TITCIC
8270	TTGACATETA TTGACATIEA	TTGACATITA	TTGACATTT	8360	TATAGAAGG2 TATAGAAGG3	TATAGAAGG	TATAGAAGG	8450	TTATGCCIG	TIATGCCIG	TIAIGCCIG
8260	CCTTCAAATC CCTTCAAATC	CCITCABAIC	 CCTTCAAATC	8350	CAATCCAGAC CAATCCAGAC 	ITCIIIIACAAICCAGACIAIAGAAGGAAAITCA	CAATCCAGAC	8440	IAACGGAAGT IAACGGAAGT	CCITACACCIAACGGAAGTITATGCCIGIT	 IAACGGAAGT
8250	AGAAGIICII AGAAGIICII	AGAAGTICIT		8340	ETTCTTTA ETTCTTTA	-8-4		8430	CIGACCAATICCCACCICIGCCITACACCIAACGGAAGIITAIGCCIGIT CIGACCAATICCCACCICIGCCITACACCIAACGGAAGTITAIGCCIGIT	SCCIIACACC	GCTTACACC'
8240	ATAMGCAMCCA ATAMGCAMCCA	TAAGCAACCI	ATAAGCAACC	8330	CTGAAGGAT	COTGAAGGAT 	CTGAAGGAT	8420	receaecter.	receacerer	CCCACCTCT(
8230	OTTTAGOTOG	TITAGCICG	CTTTAGCTCG	8320	SCTATOTOTO SCTATOTOTO SCTATOTOTO SCTATOTOTO SCTATOTOTO SCTATOTOTO SCTATOTOTOTO SCTATOTOTOTOTOTO SCTATOTOTOTOTOTOTOTOTO SCTATOTOTOTOTOTOTOTOTOTOTOTOTOTOTOTOTOTOT	TCCTATGAAGCTATCTCTGCCTGAAGGATI	CTATCTCTG	8410	ACTGACCAAT ACTGACCAAT	ACTGACCAAT	
8220	AGGATTATTC AGGATTATTC	AGGATTATTOCTITAGCTCGATAAGCAACCAGAAGTTCTTCCITCAAATCTTGACATITAATCAAT	 AGGATTATTCCTTTAGCTCGATAAGCAACCAGAAGTTCTTCCTTC	8310	TICCIAIGAAGCIAICICIGCOIGAAGGAITITICIIIIACAAICCAGACIAIAGAAATICA IICCIAIGAAGCIAICICIGCOIGAAGGATITIICIIIIACAAICCAGACIAIAGAAGGAAAIICA	ITCCTATGAA		8400	TCAGAGITITACTGACCAATICCCACCTCTGCCTTACACCTAACGGAAGITTATGCCTGTTTT TCAGAGITITACTGACCAATICCCACCTCTGCCTTAGACCTAACGGAAGITTATGCCTGTTTT	CAGAGITIL	
8210	rggggaaaat rggggaaaat 	IGGGGAAAAI.		8300	3GAAAACTGT 3GAAAACTGT 	GGAAAACTGT 		8390	CCICCATIGG	CICCATIGG	CCTCCATTGG
8200	rcagrearad rcagrearag	CAGICATAG	 FCAGTCATAG	8290	ATTOATTTT	ATTGATTTTT 		8380	EGGACTITCA EGGACTITCA	IGGACTITCA	
(8191) 8191	SEQ ID NO 11(8191) TATATTCAGTCATAGTGGGGAAAATAGGATTATTCCTTTAGCTCGATAAGCAACCAGAAGTTCTTCCTTC	SEQ ID NO 16 (688) TATATICASICATAGIGGGGAAAAT. SEQ ID NO 15 (558)	SEQ ID NO 17 (367)	(8282) 8282	SEQ ID NO 11(8282) CAGAAATTGATTTTTGGAAAACTGT SEQ ID NO 10(2755) CAGAAATTGATTTTTGGAAAACTGT SEO ID NO 13 (306)	SEQ ID NO 16 (779) CAGARAITGAITITTGGAARACIGT SEQ ID NO 15 (558)	SEQ ID NO 17 (367)	(8373) 8373	SEQ ID NO 11(8373) CAACCIGGACITICACCICCAITGGICAGAGTITI SEQ ID NO 10(2846) CAACCIGGACIITCACCICCAIIGGICAGAGTITI SEO ID NO 13 (306)	SEQUENCIS (909) SEQUENCIS (909) SEQUENCIS (868)	SEQ ID NO 17 (367)

Section 94 8554	TOACCT	IGACCI 	TIGACCT	8645	0.000 TC		 AGAGGTC Section 96	8736	STITIS VITIS		 ATTTA
	GGTTGTTATTATTAAGCATCTTTTATTTTGTGGCCTCTGATTACATGGTCCCCTAAATTTTGACCT GGTTGTTATTATTAAGCATCTTTTATTTTGTGGCCTCTGATTACATGGTCCCCTAAATTTTGACCT	GGTIGTTATTATTAAGGATGITTTATTTTGIGGCCTCTGAATTACATGGTCCCCTAAATTTTGACCT		8630	TTAACATATTAATAATATTTTGITTATGIGCCACATATCTTAGCATGTATCAATTAAGACAGAGGTC TTAACATATTAATAATATTTGITTATGIGCCAATATCTTAGCATGTATCAATTAAGACAGAGGTC	TAGGATGTATCAATTAAGACAGGTG		8720	TATTAGGATICAGAGATATTAAGAGATICTCCCAGGATCACAGITAGGTAACAGAGCIGGATTTA TATTAGGATICAGAGATATTAAGAGATICTCCCAGGATQAGAGTTAGGTAACAGAGCIGGATTTTA		
8530	GATTACATO GATTACATG		GATTACATGO	8620	TIAGCAIGI	TTAGORTGT/	TTAGCATGT	8710	CACAGITAG CACAGITAG	CACAGTIAG	
8520	TOLODODLDL.	TGTGGCCTCT	TGIGGCCICI	8610	TGTCAATATC TGTCAATATC	TATG:G:CAATATCT	TGTCAATATC	8700	CICCCAGGAI	11	CTCCAGGAT
8510	GGTTGTTATTATCAGCATCTTTTATTT GGTTGTTATTATTAAGCATCTTTTATTT		 TCTTTTATTT	8600	TITGILIAIS	AITICITIATS 		8690	TTAAGAGATI TTAAGAGATI	TAGGAITCAGAGATAITAAGAGATIC	 TTAAGAGATT
8500	TIATTAAGCA TTATTAAGCA	TTATTAAGCA 	 TTATTAAGCA	8590	TTAACATATTAATATT TTAACATATTAATAATT	TAACATATAATAATA 	TTAATAT	8680	TATTAGGATTCAGAGATATTAAGAGAT TATTAGGATTCAGAGATATTAAGAGAT	TTCAGAGATA	 TTCAGAGATA
8490	ATGGTTGTTA AIGGTTGTTA	#186118114	ΙÜ	8580	TCTTAACATA	-4	[⊢	8670	AATATTAGGA AATATTAGGA	{-+ st; {-+	
8480	ACAGITACAA. 8CAGITACAA.		 ACAGTTACAA	8570	IGGTAAAAIT	TGGTAAAATT 	IGGTAAAATT	8660	TTTGAAAGAG. TYTGAAAGAG.	TTGAAAGAG	 TTTGAAAGAG
8470	CATACCCCA. CATACCCCA		catacccaa	8560	SCRARAGAT SCRARAGAT	40744464II			OGTICICITY	H H H H H H H H H H	CGIICICII
(8464) 8464 8470	ID NO 11(8464) TTCA(ID NO 10(2937) TTCA(ID NO 10(2937)	ID NO 16 (961) TTCA ID NO 15 (558)	Onsensus(8464) TICACATACCCCAACAGTTACAAAT	(8555) 8555	ID NO 11(8555) AATO ID NO 10(3028) AATO ID NO 13 (306)	ID NO 16(1052) 8.8.7.2.3.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1	OID NO 17 (367)	(8646) 8646	ID NO 11(8646) TTAE ID NO 10(3119) TTAE ID NO 12 (206)	ID NO 15 (506) ID NO 16(1143) 打下AA(ID NO 15 (558)	3 ID NO 17 (367)
(8464) 8464	SEQ ID NO 11(8464) TECACATACCCCAACAGTTACAAAT SEQ ID NO 10(2937) TECACATACCCCAACAGTTACAAAT	SEQ ID NO 15 (961) TICACATACCCCAACAGITACAATI SEQ ID NO 16 (961) TICACATACCCCAACAGITACAATI SEQ ID NO 15 (558)	SEQ ID NO 17 (367) Consensus(8464) TTCACATAC	(8555) 8555	SEQ ID NO 11(8555) AATCACAAAAGATTGGTAAAATTTC SEQ ID NO 10(3028) AATCACAAAAGATTGGTAAAATTTC SEO ID NO 13 (306)	SEQ ID NO 16 (1052) AATCACAAAGATTGGTAAATTTC SEO ID NO 16 (558)	SEQ ID NO 17 (367) Consensus(8555) AAT	(8646) 3646	SEQ ID NO 11(8646) TTAACGTTCTCTTTTTGAAAGAGAA SEQ ID NO 10(3119) TTAACGTTCTCTTTTTGAAAGAGAA SEO ID NO 19 /906)	SEQ ID NO 15 (300)SEQ ID NO 16(1143) TIMACGITCICITITIGAAAGAGAA SEO ID NO 15 (558)	SEQ ID NO 17 (367) Consensus(8646) TIAACGIT

Section 97	CTAAGTCA	CIRAGICA	 CTAAGTCA — Section 98	8918	AATCACCA AATCACCA	<i>Crariorca</i> 	AATCACCA Section 99	6006	TACAAAAGCAG TACAAAAGCAG	 &&&&&&&	 AAAAGCAG
8810	GTATATACACCCTTTGTATAACATGTCACGAATTCAGCATAAAGGGATCTTCAGTGATCTAAGTCA GTATATACACCCTTTGTATAACATGTCACGAATTCAGCATAAAGGGATCTTCAGTGATCTAAGTCA	IAIATAGACCOITISIATAACAISICACGAATICAGGATAAAGGGATGTICAGIGAIGTAAGIGA		8900	gaccaaatagtaatatticaggctitgiggaccctatggictctatcataactgitcaaatcacca gaccaaatagtaatatticaggctitgiggaccctatggictctatcataactgitcaaatcaca	ACCCIAIGGICICIAICATAACIGIICA		8990	TAACICITTATITACAAAAGCAG TAACICITTATITACAAAAGCAG	Tranctotitattiacaraecag	
RROO	CAGCATAAAGG CAGCATAAAGG	CAGUATAAAGG	CAGCATAAAGG	8890	TATGGICICIA TATGGICICIA	TATGGTCTCTA	TATGGTCTCTA	8980	TITATGGGATTITITITA TITATGGGATTITITA	 ATGGGATITITITIA	
8790	TGTCACGAAIT	TGTCACGAATI	TGTCACGAATT	8880	GACCAAATAGTAATTTCAGGCTTIGIGGACCCTATGGTCTCT GACCAAATAGTAATATTTCAGGCTTTGIGGACCCTATGGTCTCT	TCAGGCTTTGTGBACCC	TTTGTGGACCC	8970	AAATATAAASTAASSAATGTGGCTGITITATGGGATITITITT AAATATAAASTAASSAATGTGGCTGITITATGGGATUTTITT	6-4 6-4 6-4	
8780	TTGTATAACA TTGTATAACA	TIGIAIAACA 	TTGIAIAACA	8870	TATTTCAGGC TATTTCAGGC	{ 	TATTCAGGC	8960	aaatataaactaacgaatgtggctgt aaatataaactaacgaatgtggctgt	AATAKAACTAACGAATGTGGCTGT	
8770	GTATATACACCCTT	Tatacaccet	TATACACCCT	8860	caaatagtaa caaatagtaa	GACCAAATAGTAATA	 CAAATAGTAA	8950	<i>tataaactaa</i> tataaactaa	TATAAACIAA	
8760	CTCTAACGTA CTCTAACGTA	(3)	CTCTAACGIA	8850	Taaaaaggag Taaaaaggag	 Taaaaaggac 	TAAAAGGAC	8940	ataagcaaaa ataagcaaaa	KI	
8750	CTGTCTACAG CTGTCTACAG	CIGICIACAG	 CTGTCTACAG	8840	CAACCTTTTC CAACCTTTTC	CAACCITIIC 	CAACCITITC	8930	AAAAGGAGCC AAAAGGAGCC	AAAAGGAGCC	
(8737)	SEQ ID NO 11(8737) GTCCAGGTCTGTCTACAGGTCTAAAC SEQ ID NO 10(3210) GTCCAGGTCTGTCTACAGGTCTAAC SEO ID NO 13 (306)	SEQ ID NO 16(1234) GTCCAGGTCTGTCTACAGCTCTAAC SEQ ID NO 15 (558)	SEQ ID NO 17 (367)	(8828) 8828	SEQ ID NO 11(8828) GGGGTCAGCAACCTTTTCTAAAAG SEQ ID NO 10(3301) GGGGTCAGCAACCTTTTCTAAAAG SEO ID NO 13 (306)	SEQ ID NO 16(1325) GGGGTCAGCAACCTTTCTAAAAS SEQ ID NO 15 (558)	SEQ ID NO 17 (367)	(8919) 8919	SEQ ID NO 11(8919) TGTAGTGTAAAAGGAGCCATAAGGA SEQ ID NO 10(3392) TGTAGTGTAAAAGGAGCCATAAGCA SEO ID NO 19 (206)	SEQ ID NO 15 (500)SEQ ID NO 16(1416) TGTASTSTAAAAGGAGCCATAAGGA SEO ID NO 45 (550)	SEQ ID NO 17 (367)SEQ ID NO 17 (367)

Section 100	3100	1	7	TGTGACT	9191	IGAAAT IGAAAI 	ISARAT 	 GTGAAAT Section 102	9282	TAGGCA	& U U & E	A C C C C C C C C C C C C C C C C C C
S	റമറമ	ATTIAGACT ATTIAGACT 	-	ATTTAGACT	9180	AATGATAAG AATGATAAG 	aatgatars 	 AATGATAAG S	9270	CTICIESCI		
0000	0006	TIATGGACACATTIAGACTGTGACT TTATGGACACATTIAGACTGTGACT] {	ATGGACAAC	9170	TOTEGTTT	TCTGGTGTT	TCTGGTGTT	9260	ATGICIGGA	ATCICICO	
0200	0 / 06	CCATAGNICICTORGACCOGGACORGAGAAATCINANAN FIATGGACAACANTIAGACTGTGACT CCATAGNICICTGACCCCTGACCTGAGAAAATCITATATTTATGGACACATNIAGACTGGACTG 		CCATAGIICICIGACCCTGACCIGAGAAAICITAIAIITAIGGACAACAIITAGACIGIGACI — Section 101	9160	CAACTGAAGGTCAAGGCTGGAGTTCTGAAAGCAAAGAGCTGTCTGGTGTTAATGATAAGTGAAAT CAACTGAAGGTCAAGGCTGGAGTTCTGAAAGCAAAGAGCTGTCTGGTGTTAATGATAAGTGAAAT	CAACTGAAGGICAAGGCIGGAGIICIGAAAGCAAAGAGCIGICIGGIGIIAAIGAIAAAAAAAA		9250	CCIGAACAAGAAIGICIGGACIIUTGGCII CCIGAACAAGAAIGICIGGACIICIGGCII	AAGAATAATGACCATAGACTCCIGAACAAGAATGTCTGGACTTOTGGCTTAGGCA	
Ogoo	റ്റെട	ACCTGAGAAA ACCTGAGAAA ACCTGAGAAA	######################################	ACCIGAGAAA	9150	AGTTCTGAAA AGTTCTGAAA	AGTTOTSAAA	 AGTTCTGAAA	9240	ACCATAGACT ACCATAGACT		
0080	ncna	TTGACCCCTG	5 3 3 3 5 5 6 7 8 8 9	TGACCCCTG	9140	CAAGGCTGG CAAGGCTGG	CAAGGCIGG.		9230	argaataatg. Magaataatg	AGBATABTG.	
0,00	0400	CCATAGNICTCTGACCCTGACCTGAGAAATCTTANAT CCATAGNICTCTGACCCCTGACCTGAGAAATCTTATAT 		CATAGIICIC	9130	2440TGAAGG	CAACTGAAGSI	 CAACTGAAGGT	9220	AAGAAGCACAAAAGAATAATGACCATAGACT AAGAAGCACAAAGAATAATGACCATAGACT		
0000		CACTFATGGGC		CACTTATGGG	9120	SAAGCICIGI SAAGCICIGI SAAGCICIOI	(4 (5) (4	SAAGCTCTGT	9210	roccastrat/ roccastrat/	CCCAGIIAI	- 1 €
0000	OZOG	BATCAGAACTC	68.4 C. 8.6 8.8 C. 1. C.	BATCAGAACTO	9110	TAAGAACAA(TAAGAACAA(aagtaagaacaa: 	 3TAAGAACAA(9200	GETTAGAAGAT GETTAGAAGAT	1011ACAAGA	
0,000	(2010)	SEQ ID NO 11(9010) GTGGCAGATCAGAACTCACTTATGGG SEQ ID NO 10(3483) GTGGCAGATCAGAACTCACTTATGGG SEQ ID NO 13 (306)	SEQ ID NO 18(1907) STEGSCASSALCASSACICACLLAISES SEQ ID NO 15 (558)SEQ ID NO 17 (367)	Consensus(9010) GIGGCAGAICAGAACICACIIAIGGG	(9101) 9101	SEQ ID NO 11(9101) TGCCAAGTAAGAACAAGAAGCTCTGTCAACTGAAGGTCAAGGCTGGAGTTCTGAAAGCAAAGAGCTGTCTGGTGTTAATGATAAGTGAAAT SEQ ID NO 10(3574) TGCCAAGTAAGAACAAGAAGACTCTGTCAACTGAAGGTCAAGGCTGGAGTTCTGAAAGCAAAGAGCTGTCTGGTGTTAATGATAAGTGAAAT SEO ID NO 13 (306)	SEQ ID NO 16(1598) TGCCAAGTAAGAACAAGAAGCTC SEQ ID NO 15 (558)	SEQ ID NO 17 (367)	(9192) 9192	SEQ ID NO 11(9192) AGTTAAAGTTAGAAGATCCCAGTTATAAGAAGCACAAAAAATAATGACCATAGACTCCTGAACAAGAATGTCTGGACTTGTGGCTTAGGCA SEQ ID NO 10(3665) AGTTAAAGTTAGAAGATCCCAGTTATAAGAAGCACAAAGAATAATGACCATAGACTGCTGAAGAATGTGTGGACTTGGGTTAGGCA SEO ID NO 13 (2008)	SEQ ID NO 15 (300)	SEQ ID NO 17 (367)
		SEQ ID N SEQ ID N SEQ ID N	SEQ D N	Conse		SEQ ID N SEQ ID N	SEQ ID N SEQ ID N	SEQ ID N		SEQ ID N		SEQ ID N

, , , ,		9290	9300	9310	9320	9530	0.45g	9350	9360	9373
SEQ ID NO 11(9283) CECTIGITGIA EGECCAGGCCAAGIT SEQ ID NO 10(3756) CECTIGITGIA EGECCAGGCCAAGIT		TGTATGGT TGTATGGT(CCAGGCCAA(STIACCIAAIC	TCTCCAGGC	CICCALITI	CTIAICALTA CITAICALTA	aatgaagataa aatgaagataa	SEQ ID NO 11(9283) OTOTIGITGITGITCAGGCCAAGITACCIAATCICICCAGGCCICCATTITCITAICATTAAATGAAGATAAAAGTAITTICCICA SEQ ID NO 10(3756) OTOTIGITGITGITCAGGCCAAGITACCIAATCICICCAGGCCICCATTICITAICATTAAATGAAGATAAAAGTAITTICITA	TOGTO
SEQ ID NO 13 (306)		TGTATGGT(STIACCTAATC	10 10 C \$ C C C C C C C C C C C C C C C C C	CICCATII	CITAICATIA	AATGAAGATAA 	ACCTAATOIOTOCAGGCCTCCATITICITATCATTAAATGAAGAIAATAAAAGIAITTTCCTCA	
SEQ ID NO 17 (367) Consensus(9283) CTCTTGT	ICITGI	 TGTATGGTC	ccaggccaag	GITACCTAATC	TCTCCAGGC	CICCATITIC	CTTATCATTA	 AATGAAGATAAT	 AAAAGTATT	 TTCCTCA Section 104
(9374) 93	(9374) 9374 9380	180	9390	9400	9410	9420	9430	9440	9458	
SEQ ID NO 11(9374) GAGAGCTGTAAGAATAAACTGAGCTAA SEQ ID NO 10(3847) GAGAGCTGTAAGAATAAACTGAGCTAA	AGAGCT	STAAGAAT. STAAGAAT!	AAACIGAGC AAACIGAGC	TAACCCATGTC FAACCCATGTC	AAGCACAIA AAGCACAIA	GAATAGGGC GAATAGGGC	CCAGCCTATA CCAGCCTATA	TIAATITATO? TIAATITATOA	SEQ ID NO 11(9374) GAGAGCIGIAAGAATAAACTGAGCTAACCCATGTCAAGCACATAGAATAGGGCCCAGGCTATATTAATTTATCAATAAATGCCAG SEQ ID NO 10(3847) GAGAGCTGTAAGAATAAACTGAGCTAACCCATGTCAAGCACATAGAATAGGGCCCAGGCCTATATTAATTTATCAATAAATGCCAG	
SEQ ID NO 16(1871) GAGAGCISIAAGAAIAAACIGAGCIAAA	EUSKS.	 SIAAGAAI	AAACIGAGC	 BACCCATGIC	ARGCACAIA	GAATAGGGC	CORSCOIRTR	TIAATITAICA		
SEQ ID NO 15 (558)										